



SEQUENCE LISTING

<110> Raymond J. Dattwyler
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Maria J.C. Gomes-Solecki

<120> Groups of *Borrelia Burgdorferi* and
Borrelia Afzelii That Cause Lyme Disease In Humans

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<140> 09/596,746
<141> 2000-06-19

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<151> 1999-06-18

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gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 20 25 30

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144
 Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
 35 40 45

ttg ctg tca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata 192
 Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile
 50 55 60

aaa aac gat ggt agt tta gat aat gaa gca aat cgc aac gag tca ttg 240
 Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu
 65 70 75 80

tta gca gga gct tat aca ata tca acc tta ata aca caa aaa tta agt 288
 Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser
 85 90 95

aaa tta aac gga tca gaa ggt tta aag gaa aag att gcc gca gct aag 336
 Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys
 100 105 110

aaa tgc tct gaa gag ttt agt act aaa cta aaa gat aat cat gca cag 384
 Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln
 115 120 125

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ctt ggt ata cag ggc gtt act gat gaa aat gca aaa aaa gct att tta 432
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 130 135 140

aaa gca aat gca gcg ggt aaa gat aag ggc gtt gaa gaa ctt gaa aag 480
 Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys
 145 150 155 160

ttg tcc gga tca tta gaa agc tta tca aaa gca gct aaa gag atg ctt 528
 Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu
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<213> borrelia burgdorferi

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 50 55 60
 Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu
 65 70 75 80
 Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser
 85 90 95
 Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys
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 Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln
 115 120 125
 Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu
 130 135 140
 Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys
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att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa gtt gag acc	144
Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr	
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tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aaa aaa	192
Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys	
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65 70 75 80	
tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta aat	288
Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn	
85 90 95	
gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag caa	336
Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln	
100 105 110	
tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat gca gtg ctt	384
Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu	
115 120 125	
ggt ctg gac aat ctt act gat gat aat gca caa aga gct att tta aaa	432
Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys	
130 135 140	
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Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe	
145 150 155 160	
aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa aat	528
Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn	
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Ala Val Lys Glu Leu Thr Ser Pro Ile	
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 35 40 45
 Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys
 50 55 60
 Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu
 65 70 75 80
 Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn
 85 90 95
 Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln
 100 105 110
 Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu
 115 120 125
 Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys
 130 135 140
 Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe
 145 150 155 160
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 Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu
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 aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta ctt gct 144
 Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu Ala
 35 40 45
 gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att gct gct 192
 Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala
 50 55 60

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 65 70 75 80

aat aat cac aat gga tca ttg tta gcg gga gct tat gca ata tca acc 288
 Asn Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr
 85 90 95

cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta aag gaa 336
 Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu
 100 105 110

aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat aaa tta 384
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 115 120 125

aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat gct gat 432
 Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Ala Asp
 130 135 140

gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa ggt gct 480
 Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala
 145 150 155 160

gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca aaa gca 528
 Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser Lys Ala
 165 170 175

gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc cct gtt 576
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gtg 579
 Val

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<213> *Borrelia burgdorferi*

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 35 40 45
 Val Lys Glu Val Glu Ala Leu Ser Ser Ile Asp Glu Ile Ala Ala
 50 55 60
 Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp Thr Glu
 65 70 75 80
 Asn Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr
 85 90 95
 Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu
 100 105 110
 Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu
 115 120 125

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Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Ala Asp
 130 135 140
 Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala
 145 150 155 160
 Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser Lys Ala
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 Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val
 180 185 190
 Val

<210> 11
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 aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt 96
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 20 25 30

 aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta ctt gct 144
 Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu Ala
 35 40 45

 gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt gct aaa 192
 Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys
 50 55 60

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 Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala
 65 70 75 80

 aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca acc tta 288
 Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu
 85 90 95

 ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta aag gaa 336
 Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu
 100 105 110

 aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act aaa cta 384
 Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu
 115 120 125

 aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat gaa aat 432
 Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp Glu Asn
 130 135 140

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Val	Glu	Glu	Leu	Glu	Lys	Leu	Ser	Gly	Ser	Leu	Glu	Ser	Leu	Ser	Lys	
				165					170						175	

gca	gct	aaa	gag	atg	ctt	gct	aat	tca	ggt	aaa	gag	ctt	aca	agc	cct	576
Ala	Ala	Lys	Glu	Met	Leu	Ala	Asn	Ser	Val	Lys	Glu	Leu	Thr	Ser	Pro	
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Val	Val															

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Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Asp	Ser	Asn	Ala	Val	Leu	Leu	Ala	
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Val	Lys	Glu	Val	Glu	Ala	Leu	Leu	Ser	Ser	Ile	Asp	Glu	Leu	Ala	Lys	
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Ala	Ile	Gly	Lys	Lys	Ile	Lys	Asn	Asp	Gly	Ser	Leu	Asp	Asn	Glu	Ala	
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Ile	Thr	Gln	Lys	Leu	Ser	Lys	Leu	Asn	Gly	Ser	Glu	Gly	Leu	Lys	Glu	
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Val	Glu	Glu	Leu	Glu	Lys	Leu	Ser	Gly	Ser	Leu	Glu	Ser	Leu	Ser	Lys	
			165						170					175		
Ala	Ala	Lys	Glu	Met	Leu	Ala	Asn	Ser	Val	Lys	Glu	Leu	Thr	Ser	Pro	
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aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt	96
Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu	
20 25 30	
aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gcc	144
Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala	
35 40 45	
gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt gct acc	192
Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr	
50 55 60	
aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc aat cag	240
Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln	
65 70 75 80	
agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct gac cta	288
Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu	
85 90 95	
ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag gaa aag	336
Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys	
100 105 110	
att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa cta aaa	384
Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys	
115 120 125	
agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat aat gca	432
Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala	
130 135 140	
caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt gct gca	480
Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala	
145 150 155 160	
gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa gca gct	528
Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala	
165 170 175	
caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct att gtg	576
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<210> 14
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 <213> *Borrelia burgdorferi*

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 35 40 45
 Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr
 50 55 60
 Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln
 65 70 75 80
 Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu
 85 90 95
 Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys
 100 105 110
 Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys
 115 120 125
 Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala
 130 135 140
 Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala
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 Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala
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 Asn Ala Ser Thr Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu
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 aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gcc 144
 Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala
 35 40 45
 gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt gct acc 192
 Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr
 50 55 60

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65 70 75 80

agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct gac cta 288
Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu
85 90 95

ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag gaa aag 336
Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys
100 105 110

att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa cta aaa 384
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115 120 125

agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat aat gca 432
Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala
130 135 140

caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt gct gca 480
Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala
145 150 155 160

gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa gca gct 528
Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala
165 170 175

caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct att gtg 576
Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile Val
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<210> 16
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<213> borrelia burgdorferi

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35 40 45
Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr
50 55 60
Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln
65 70 75 80
Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu
85 90 95
Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys
100 105 110
Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys
115 120 125
Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala
130 135 140

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Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala
 145 150 155 160
 Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala
 165 170 175

Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile Val
 180 185 190

<210> 17
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aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt 96
 Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu
 20 25 30

aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctc gcc 144
 Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala
 35 40 45

gtg aaa gaa gtt gaa act ttg ctt aca tct ata gat gag ctt gct aaa 192
 Val Lys Glu Val Glu Thr Leu Thr Ser Ile Asp Glu Leu Ala Lys
 50 55 60

gct att ggt aaa aaa ata aaa aac gat gtt agt tta gat aat gag gca 240
 Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala
 65 70 75 80

gat cac aac gga tca tta ata tca gga gca tat tta att tca aac tta 288
 Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu
 85 90 95

ata aca aaa aaa ata agt gca ata aaa gat tca gga gaa ttg aag gca 336
 Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala
 100 105 110

gaa att gaa aag gct aag aaa tgt tct gaa gaa ttt act gct aaa tta 384
 Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu
 115 120 125

aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc gtt act gat gat aat 432
 Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn
 130 135 140

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gca aaa aaa gcc att tta aaa aca aat aat gat aaa act aag ggc gct 480
 Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala
 145 150 155 160

gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac ttg tca aaa gca 528
 Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala
 165 170 175

gct aaa gag atg ctt act aat tca gtt aaa gag ctt aca agc cct 573
 Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser Pro
 180 185 190

<210> 18

<211> 191

<212> PRT

<213> *Borrelia burgdorferi*

<400> 18

Met Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly
 1 5 10 15
 Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu
 20 25 30
 Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala
 35 40 45
 Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys
 50 55 60
 Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala
 65 70 75 80
 Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu
 85 90 95
 Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala
 100 105 110
 Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu
 115 120 125
 Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn
 130 135 140
 Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala
 145 150 155 160
 Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala
 165 170 175
 Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser Pro
 180 185 190

<210> 19

<211> 553

<212> DNA

<213> *Borrelia burgdorferi*

<220>

<221> CDS

<222> (1)...(553)

<400> 19

atg act tta ttt tta ttt ata tct tgt aat aat tca gga aaa gat ggg	48
Met Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly	
1 5 10 15	
aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt	96
Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu	
20 25 30	
aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gct	144
Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala	
35 40 45	
gtg aaa gaa att gaa act ttg ctt gca tct ata gat gaa ctt gct act	192
Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr	
50 55 60	
aaa gct att ggt aaa aaa ata gat aac aat gct ggt ttg ggt gct gaa	240
Lys Ala Ile Gly Lys Lys Ile Asp Asn Asn Ala Gly Leu Gly Ala Glu	
65 70 75 80	
gtg ggt caa aac gga tca ttg cta gca gga gct tat gca atc tca act	288
Val Gly Gln Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr	
85 90 95	
gta ata ata gaa aaa ttg agc aca tta aaa aat gta gaa gaa tta aaa	336
Val Ile Ile Glu Lys Leu Ser Thr Leu Lys Asn Val Glu Glu Leu Lys	
100 105 110	
gaa aaa att aca aag gct aag gat tgt tct gaa aaa ttc act aaa aaa	384
Glu Lys Ile Thr Lys Ala Lys Asp Cys Ser Glu Lys Phe Thr Lys Lys	
115 120 125	
tta aaa gat agc cgc gca gag ctt ggt aaa aaa gat gcc agt gat gat	432
Leu Lys Asp Ser Arg Ala Glu Leu Gly Lys Lys Asp Ala Ser Asp Asp	
130 135 140	
gat gca aaa aaa gct att tta aaa aca aat caa gct aac gat aag ggt	480
Asp Ala Lys Lys Ala Ile Leu Lys Thr Asn Gln Ala Asn Asp Lys Gly	
145 150 155 160	
gct aaa gaa ctt aaa gag tta ttt gaa gca gta gaa agc ttg tca aaa	528
Ala Lys Glu Leu Lys Glu Leu Phe Glu Ala Val Glu Ser Leu Ser Lys	
165 170 175	
gcg gct aaa gag atg cta aac aag t	553
Ala Ala Lys Glu Met Leu Asn Lys	
180	

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<210> 20
 <211> 184
 <212> PRT
 <213> *Borrelia burgdorferi*

<400> 20
 Met Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly
 1 5 10 15
 Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu
 20 25 30
 Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala
 35 40 45
 Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr
 50 55 60
 Lys Ala Ile Gly Lys Lys Ile Asp Asn Asn Ala Gly Leu Gly Ala Glu
 65 70 75 80
 Val Gly Gln Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr
 85 90 95
 Val Ile Ile Glu Lys Leu Ser Thr Leu Lys Asn Val Glu Glu Leu Lys
 100 105 110
 Glu Lys Ile Thr Lys Ala Lys Asp Cys Ser Glu Lys Phe Thr Lys Lys
 115 120 125
 Leu Lys Asp Ser Arg Ala Glu Leu Gly Lys Lys Asp Ala Ser Asp Asp
 130 135 140
 Asp Ala Lys Lys Ala Ile Leu Lys Thr Asn Gln Ala Asn Asp Lys Gly
 145 150 155 160
 Ala Lys Glu Leu Lys Glu Leu Phe Glu Ala Val Glu Ser Leu Ser Lys
 165 170 175
 Ala Ala Lys Glu Met Leu Asn Lys
 180

<210> 21
 <211> 582
 <212> DNA
 <213> *Borrelia burgdorferi*

<220>
 <221> CDS
 <222> (1)...(582)

<400> 21
 atg act tta ttt tta ttt ata tct tgt aat aat tca gga aaa gat ggg 48
 Met Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly
 1 5 10 15
 aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt 96
 Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu
 20 25 30
 aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gct 144
 Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala
 35 40 45

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gtg aaa gaa att gaa act ttg ctt gca tct ata gat gaa ctt gct act 192
Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr
    50                55                60

aaa gct att ggt aaa aaa ata caa caa aat ggt ggt tta gct gtc gaa 240
Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu
    65                70                75                80

gcg ggg cat aat gga aca ttg tta gca ggt gct tat aca ata tca aaa 288
Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys
                85                90                95

cta ata aca caa aaa tta gat gga ttg aaa aat tca gaa aaa tta aag 336
Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys
                100                105                110

gaa aaa att gaa aat gct aag aaa tgt tct gaa gat ttt act aaa aaa 384
Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys
                115                120                125

cta gaa gga gaa cat gcg caa ctt gga att gaa aat gtt act gat gag 432
Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu
                130                135                140

aat gca aaa aaa gct att tta ata aca gat gca gct aaa gat aag ggc 480
Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly
    145                150                155                160

gct gca gag ctt gaa aag cta ttt aaa gca gta gaa aac ttg gca aaa 528
Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys
                165                170                175

gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agt cct 576
Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro
                180                185                190

att gtg
Ile Val

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582

<210> 22

<211> 194

<212> PRT

<213> *Borrelia burgdorferi*

<400> 22

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Met Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly
1      5      10      15
Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu
20     25     30
Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala
35     40     45
Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr
50     55     60
Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu
65     70     75     80

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Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys
 85 90 95
 Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys
 100 105 110
 Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys
 115 120 125
 Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu
 130 135 140
 Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly
 145 150 155 160
 Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys
 165 170 175
 Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro
 180 185 190
 Ile Val

<210> 23
 <211> 1128
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> OspC Chimera

<221> CDS
 <222> (1)...(1128)

<400> 23
 atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48
 Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
 1 5 10 15

 gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 20 25 30

 att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144
 Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
 35 40 45

 ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 192
 Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
 50 55 60

 ata cac caa aat aat ggt ttg gat acc gaa tat aat cac aat gga tca 240
 Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser
 65 70 75 80

 ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta 288
 Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
 85 90 95

 gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag 336
 Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
 100 105 110

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aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat	384
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp	
115 120 125	
ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta	432
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu	
130 135 140	
aaa aca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta	480
Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu	
145 150 155 160	
ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct	528
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala	
165 170 175	
aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca gcc	576
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala	
180 185 190	
atg gta aat aat tca ggg aaa gat ggg aat aca tct gca aat tct gct	624
Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala	
195 200 205	
gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa att	672
Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile	
210 215 220	
aca gaa tct aac gca gtt gtt ctc gcc gtg aaa gaa gtt gaa act ttg	720
Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu	
225 230 235 240	
ctt aca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata aaa	768
Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys	
245 250 255	
aac gat gtt agt tta gat aat gag gca gat cac aac gga tca tta ata	816
Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile	
260 265 270	
tca gga gca tat tta att tca aac tta ata aca aaa aaa ata agt gca	864
Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala	
275 280 285	
ata aaa gat tca gga gaa ttg aag gca gaa att gaa aag gct aag aaa	912
Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys	
290 295 300	
tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa cac aca gat ctt	960
Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu	
305 310 315 320	

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ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa gcc att tta aaa 1008
Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys
      325      330      335

aca aat aat gat aaa act aag ggc gct gat gaa ctt gaa aag tta ttt 1056
Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe
      340      345      350

gaa tca gta aaa aac ttg tca aaa gca gct aaa gag atg ctt act aat 1104
Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn
      355      360      365

tca gtt aaa gag ctt aca agc taa 1128
Ser Val Lys Glu Leu Thr Ser *
      370      375

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<210> 24
<211> 375
<212> PRT
<213> Artificial Sequence

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<220>
<223> OspC Chimera

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<400> 24
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
 1      5      10      15
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 20      25      30
Ile Thr Asp Ser Asn Ala Val Leu Ala Val Lys Glu Val Glu Ala
 35      40      45
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
 50      55      60
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser
 65      70      75      80
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
 85      90      95
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
100      105      110
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
115      120      125
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
130      135      140
Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu
145      150      155      160
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
165      170      175
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala
180      185      190
Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala
195      200      205
Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile
210      215      220
Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu
225      230      235      240

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Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys
      245      250      255
Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile
      260      265      270
Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala
      275      280      285
Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys
      290      295      300
Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu
305      310      315      320
Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys
      325      330      335
Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe
      340      345      350
Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn
      355      360      365
Ser Val Lys Glu Leu Thr Ser
      370      375

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<210> 25

<211> 1124

<212> DNA

<213> Artificial Sequence

<220>

<223> OspC Chimera

<221> CDS

<222> (1)...(1124)

<400> 25

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atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
  1              5              10              15

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
      20              25              30

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
      35              40              45

ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 192
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
      50              55              60

ata cac caa aat aat ggt ttg gat acc gaa tat aat cac aat gga tca 240
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser
      65              70              75              80

ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta 288
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
      85              90              95

gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag 336

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Asp	Gly	Leu	Lys	Asn	Glu	Gly	Leu	Lys	Glu	Lys	Ile	Asp	Ala	Ala	Lys	
			100					105					110			
aaa	tgt	tct	gaa	aca	ttt	act	aat	aaa	tta	aaa	gaa	aaa	cac	aca	gat	384
Lys	Cys	Ser	Glu	Thr	Phe	Thr	Asn	Lys	Leu	Lys	Glu	Lys	His	Thr	Asp	
		115					120					125				
ctt	ggt	aaa	gaa	ggt	gtt	act	gat	gct	gat	gca	aaa	gaa	gcc	att	tta	432
Leu	Gly	Lys	Glu	Gly	Val	Thr	Asp	Ala	Asp	Ala	Lys	Glu	Ala	Ile	Leu	
	130					135					140					
aaa	aca	aat	ggt	act	aaa	act	aaa	ggt	gct	gaa	gaa	ctt	gga	aaa	tta	480
Lys	Thr	Asn	Gly	Thr	Lys	Thr	Lys	Gly	Ala	Glu	Glu	Leu	Gly	Lys	Leu	
145					150					155					160	
ttt	gaa	tca	gta	gag	gtc	ttg	tca	aaa	gca	gct	aaa	gag	atg	ctt	gct	528
Phe	Glu	Ser	Val	Glu	Val	Leu	Ser	Lys	Ala	Ala	Lys	Glu	Met	Leu	Ala	
				165					170					175		
aat	tca	gtt	aaa	gag	ctt	aca	agc	cct	gtt	gtg	gca	gaa	agt	cca	gcc	576
Asn	Ser	Val	Lys	Glu	Leu	Thr	Ser	Pro	Val	Val	Ala	Glu	Ser	Pro	Ala	
			180					185					190			
atg	gta	aat	aat	tca	gga	aaa	gat	ggg	aat	aca	tct	gca	aat	tct	gct	624
Met	Val	Asn	Asn	Ser	Gly	Lys	Asp	Gly	Asn	Thr	Ser	Ala	Asn	Ser	Ala	
		195					200					205				
gat	gag	tct	gtt	aaa	ggg	cct	aat	ctt	aca	gaa	ata	agt	aaa	aaa	att	672
Asp	Glu	Ser	Val	Lys	Gly	Pro	Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	
	210					215					220					
aca	gaa	tct	aac	gca	gtt	gtt	ctg	gct	gtg	aaa	gaa	att	gaa	act	ttg	720
Thr	Glu	Ser	Asn	Ala	Val	Val	Leu	Ala	Val	Lys	Glu	Ile	Glu	Thr	Leu	
225					230					235					240	
ctt	gca	tct	ata	gat	gaa	ctt	gct	act	aaa	gct	att	ggt	aaa	aaa	ata	768
Leu	Ala	Ser	Ile	Asp	Glu	Leu	Ala	Thr	Lys	Ala	Ile	Gly	Lys	Lys	Ile	
				245					250					255		
caa	caa	aat	ggt	ggt	tta	gct	gtc	gaa	gca	ggg	cat	aat	gga	aca	ttg	816
Gln	Gln	Asn	Gly	Gly	Leu	Ala	Val	Glu	Ala	Gly	His	Asn	Gly	Thr	Leu	
			260					265					270			
tta	gca	ggt	gct	tat	aca	ata	tca	aaa	cta	ata	aca	caa	aaa	tta	gat	864
Leu	Ala	Gly	Ala	Tyr	Thr	Ile	Ser	Lys	Leu	Ile	Thr	Gln	Lys	Leu	Asp	
		275					280					285				
gga	ttg	aaa	aat	tca	gaa	aaa	tta	aag	gaa	aaa	att	gaa	aat	gct	aag	912
Gly	Leu	Lys	Asn	Ser	Glu	Lys	Leu	Lys	Glu	Lys	Ile	Glu	Asn	Ala	Lys	
	290					295					300					
aaa	tgt	tct	gaa	gat	ttt	act	aaa	aaa	cta	gaa	gga	gaa	cat	gca	caa	960
Lys	Cys	Ser	Glu	Asp	Phe	Thr	Lys	Lys	Leu	Glu	Gly	Glu	His	Ala	Gln	
305					310					315					320	

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ctt gga att gaa aat gtt act gat gag aat gca aaa aaa gct att tta 1008
 Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu
 325 330 335

ata aca gat gca gct aaa gat aag ggc gct gca gag ctt gaa aag cta 1056
 Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu
 340 345 350

ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa gag atg ctt gct 1104
 Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala
 355 360 365

aat tca gtt aaa gag ctt ac 1124
 Asn Ser Val Lys Glu Leu
 370

<210> 26

<211> 374

<212> PRT

<213> Artificial Sequence

<220>

<223> OspC Chimera

<400> 26

Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
 1 5 10 15
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 20 25 30
 Ile Thr Asp Ser Asn Ala Val Leu Ala Val Lys Glu Val Glu Ala
 35 40 45
 Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
 50 55 60
 Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser
 65 70 75 80
 Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
 85 90 95
 Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
 100 105 110
 Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
 115 120 125
 Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
 130 135 140
 Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu
 145 150 155 160
 Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
 165 170 175
 Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala
 180 185 190
 Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala
 195 200 205
 Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile
 210 215 220
 Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu
 225 230 235 240

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Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile
 245 250 255
 Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu
 260 265 270
 Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp
 275 280 285
 Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys
 290 295 300
 Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln
 305 310 315 320
 Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu
 325 330 335
 Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu
 340 345 350
 Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala
 355 360 365
 Asn Ser Val Lys Glu Leu
 370

<210> 27

<211> 1137

<212> DNA

<213> Artificial Sequence

<220>

<223> OspC Chimera

<221> CDS

<222> (1)...(1137)

<400> 27

atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct	48
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser	
1 5 10 15	
gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata aat aaa aaa	96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys	
20 25 30	
att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg	144
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala	
35 40 45	
ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa	192
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys	
50 55 60	
ata cac caa aat aat ggt ttg gat acc gaa aat aat cac aat gga tca	240
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser	
65 70 75 80	
ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta	288
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu	
85 90 95	

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gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag	336
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys	
100 105 110	
aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat	384
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp	
115 120 125	
ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta	432
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu	
130 135 140	
aaa gca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta	480
Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu	
145 150 155 160	
ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct	528
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala	
165 170 175	
aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca aaa	576
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys	
180 185 190	
aaa cct tcc atg gta aat aat tca ggg aaa gat ggg aat aca tct gca	624
Lys Pro Ser Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala	
195 200 205	
aat tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt	672
Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser	
210 215 220	
aaa aaa att aca gaa tct aac gca gtt gtt ctc gcc gtg aaa gaa gtt	720
Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val	
225 230 235 240	
gaa act ttg ctt aca tct ata gat gag ctt gct aaa gct att ggt aaa	768
Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys	
245 250 255	
aaa ata aaa aac gat gtt agt tta gat aat gag gca gat cac aac gga	816
Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly	
260 265 270	
tca tta ata tca gga gca tat tta att tca aac tta ata aca aaa aaa	864
Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys	
275 280 285	
ata agt gca ata aaa gat tca gga gaa ttg aag gca gaa att gaa aag	912
Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys	
290 295 300	
gct aag aaa tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa cac	960
Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His	
305 310 315 320	

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```

aca gat ctt ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa gcc 1008
Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala
      325              330              335

att tta aaa aca aat aat gat aaa act aag ggc gct gat gaa ctt gaa 1056
Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu
      340              345              350

aag tta ttt gaa tca gta aaa aac ttg tca aaa gca gct aaa gag atg 1104
Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met
      355              360              365

ctt act aat tca gtt aaa gag ctt aca agc taa 1137
Leu Thr Asn Ser Val Lys Glu Leu Thr Ser *
      370              375

```

```

<210> 28
<211> 378
<212> PRT
<213> Artificial Sequence

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<220>
<223> OspC Chimera

```

```

<400> 28
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
 1          5          10          15
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys
 20          25          30
Ile Thr Asp Ser Asn Ala Val Leu Ala Val Lys Glu Val Glu Ala
 35          40          45
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
 50          55          60
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser
 65          70          75          80
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
 85          90          95
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
100          105          110
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
115          120          125
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
130          135          140
Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu
145          150          155          160
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
165          170          175
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys
180          185          190
Lys Pro Ser Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala
195          200          205
Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser
210          215          220
Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val
225          230          235          240

```

<400>	29																
atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct	48																
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser																	
1 5 10 15																	
gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata aat aaa aaa	96																
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys																	
20 25 30																	
att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg	144																
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala																	
35 40 45																	
ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa	192																
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys																	
50 55 60																	
ata cac caa aat aat ggt ttg gat acc gaa aat aat cac aat gga tca	240																
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser																	
65 70 75 80																	
ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta	288																
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu																	
85 90 95																	
gat qga ttg aaa aat qaa qga tta aaq qaa aaa att gat gcg gct aag	336																

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Asp	Gly	Leu	Lys	Asn	Glu	Gly	Leu	Lys	Glu	Lys	Ile	Asp	Ala	Ala	Lys	
			100					105					110			
aaa	tgt	tct	gaa	aca	ttt	act	aat	aaa	tta	aaa	gaa	aaa	cac	aca	gat	384
Lys	Cys	Ser	Glu	Thr	Phe	Thr	Asn	Lys	Leu	Lys	Glu	Lys	His	Thr	Asp	
		115					120					125				
ctt	ggt	aaa	gaa	ggt	gtt	act	gat	gct	gat	gca	aaa	gaa	gcc	att	tta	432
Leu	Gly	Lys	Glu	Gly	Val	Thr	Asp	Ala	Asp	Ala	Lys	Glu	Ala	Ile	Leu	
	130					135					140					
aaa	gca	aat	ggt	act	aaa	act	aaa	ggt	gct	gaa	gaa	ctt	gga	aaa	tta	480
Lys	Ala	Asn	Gly	Thr	Lys	Thr	Lys	Gly	Ala	Glu	Glu	Leu	Gly	Lys	Leu	
145					150					155					160	
ttt	gaa	tca	gta	gag	gtc	ttg	tca	aaa	gca	gct	aaa	gag	atg	ctt	gct	528
Phe	Glu	Ser	Val	Glu	Val	Leu	Ser	Lys	Ala	Ala	Lys	Glu	Met	Leu	Ala	
				165					170					175		
aat	tca	gtt	aaa	gag	ctt	aca	agc	cct	gtt	gtg	gca	gaa	agt	cca	aaa	576
Asn	Ser	Val	Lys	Glu	Leu	Thr	Ser	Pro	Val	Val	Ala	Glu	Ser	Pro	Lys	
			180					185					190			
aaa	cct	tcc	atg	gta	aat	aat	tca	gga	aaa	gat	ggg	aat	aca	tct	gca	624
Lys	Pro	Ser	Met	Val	Asn	Asn	Ser	Gly	Lys	Asp	Gly	Asn	Thr	Ser	Ala	
		195					200					205				
aat	tct	gct	gat	gag	tct	gtt	aaa	ggg	cct	aat	ctt	aca	gaa	ata	agt	672
Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro	Asn	Leu	Thr	Glu	Ile	Ser	
	210					215					220					
aaa	aaa	att	aca	gaa	tct	aac	gca	gtt	gtt	ctg	gct	gtg	aaa	gaa	att	720
Lys	Lys	Ile	Thr	Glu	Ser	Asn	Ala	Val	Val	Leu	Ala	Val	Lys	Glu	Ile	
225					230					235					240	
gaa	act	ttg	ctt	gca	tct	ata	gat	gaa	ctt	gct	act	aaa	gct	att	ggt	768
Glu	Thr	Leu	Leu	Ala	Ser	Ile	Asp	Glu	Leu	Ala	Thr	Lys	Ala	Ile	Gly	
				245					250					255		
aaa	aaa	ata	caa	caa	aat	ggt	ggt	tta	gct	gtc	gaa	gcg	ggg	cat	aat	816
Lys	Lys	Ile	Gln	Gln	Asn	Gly	Gly	Leu	Ala	Val	Glu	Ala	Gly	His	Asn	
			260					265					270			
gga	aca	ttg	tta	gca	ggt	gct	tat	aca	ata	tca	aaa	cta	ata	aca	caa	864
Gly	Thr	Leu	Leu	Ala	Gly	Ala	Tyr	Thr	Ile	Ser	Lys	Leu	Ile	Thr	Gln	
		275					280					285				
aaa	tta	gat	gga	ttg	aaa	aat	tca	gaa	aaa	tta	aag	gaa	aaa	att	gaa	912
Lys	Leu	Asp	Gly	Leu	Lys	Asn	Ser	Glu	Lys	Leu	Lys	Glu	Lys	Ile	Glu	
	290					295					300					
aat	gct	aag	aaa	tgt	tct	gaa	gat	ttt	act	aaa	aaa	cta	gaa	gga	gaa	960
Asn	Ala	Lys	Lys	Cys	Ser	Glu	Asp	Phe	Thr	Lys	Lys	Leu	Glu	Gly	Glu	
305					310					315					320	

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```

cat gcg caa ctt gga att gaa aat gtt act gat gag aat gca aaa aaa 1008
His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys
      325      330      335

gct att tta ata aca gat gca gct aaa gat aag ggc gct gca gag ctt 1056
Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu
      340      345      350

gaa aag cta ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa gag 1104
Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu
      355      360      365

atg ctt gct aat tca gtt aaa gag ctt ac 1133
Met Leu Ala Asn Ser Val Lys Glu Leu
      370      375

```

```

<210> 30
<211> 377
<212> PRT
<213> Artificial Sequence

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<220>
<223> OspC Chimera

```

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<400> 30
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
 1      5      10      15
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys
 20      25      30
Ile Thr Asp Ser Asn Ala Val Leu Ala Val Lys Glu Val Glu Ala
 35      40      45
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
 50      55      60
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser
 65      70      75      80
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
 85      90      95
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
100      105      110
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
115      120      125
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
130      135      140
Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu
145      150      155      160
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
165      170      175
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys
180      185      190
Lys Pro Ser Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala
195      200      205
Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser
210      215      220
Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile
225      230      235      240

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Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly
 245 250 255
 Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn
 260 265 270
 Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln
 275 280 285
 Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu
 290 295 300
 Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu
 305 310 315 320
 His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys
 325 330 335
 Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu
 340 345 350
 Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu
 355 360 365
 Met Leu Ala Asn Ser Val Lys Glu Leu
 370 375

<210> 31
 <211> 1112
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> OspC Chimera

 <221> CDS
 <222> (1)...(1112)

<400> 31
 atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48
 Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
 1 5 10 15

 gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 20 25 30

 att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144
 Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
 35 40 45

 ttg ctg tca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata 192
 Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile
 50 55 60

 aaa aac gat ggt agt tta gat aat gaa gca aat cgc aac gag tca ttg 240
 Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu
 65 70 75 80

 tta gca gga gct tat aca ata tca acc tta ata aca caa aaa tta agt 288
 Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser
 85 90 95

 aaa tta aac gga tca gaa ggt tta aag gaa aag att gcc gca gct aag 336

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Lys	Leu	Asn	Gly	Ser	Glu	Gly	Leu	Lys	Glu	Lys	Ile	Ala	Ala	Ala	Lys		
			100					105					110				
aaa	tgc	tct	gaa	gag	ttt	agt	act	aaa	cta	aaa	gat	aat	cat	gca	cag	384	
Lys	Cys	Ser	Glu	Glu	Phe	Ser	Thr	Lys	Leu	Lys	Asp	Asn	His	Ala	Gln		
		115					120					125					
ctt	ggt	ata	cag	ggc	gtt	act	gat	gaa	aat	gca	aaa	aaa	gct	att	tta	432	
Leu	Gly	Ile	Gln	Gly	Val	Thr	Asp	Glu	Asn	Ala	Lys	Lys	Ala	Ile	Leu		
	130					135					140						
aaa	gca	aat	gca	gcg	ggt	aaa	gat	aag	ggc	gtt	gaa	gaa	ctt	gaa	aag	480	
Lys	Ala	Asn	Ala	Ala	Gly	Lys	Asp	Lys	Gly	Val	Glu	Glu	Leu	Glu	Lys		
145					150				155						160		
ttg	tcc	gga	tca	tta	gaa	agc	tta	tca	aaa	gca	gct	aaa	gag	atg	ctt	528	
Leu	Ser	Gly	Ser	Leu	Glu	Ser	Leu	Ser	Lys	Ala	Ala	Lys	Glu	Met	Leu		
			165					170						175			
gct	aat	tca	gtt	aaa	gag	ctt	aca	agc	cct	gtt	gtc	cat	ggt	aat	aat	576	
Ala	Asn	Ser	Val	Lys	Glu	Leu	Thr	Ser	Pro	Val	Val	His	Gly	Asn	Asn		
			180				185						190				
tca	aga	aaa	gat	ggg	aat	gca	tct	aca	aat	tct	gcc	gat	gag	tct	gtt	624	
Ser	Arg	Lys	Asp	Gly	Asn	Ala	Ser	Thr	Asn	Ser	Ala	Asp	Glu	Ser	Val		
		195					200					205					
aaa	ggg	cct	aat	ctt	aca	gaa	ata	agt	aaa	aaa	att	aca	gaa	tct	aac	672	
Lys	Gly	Pro	Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Glu	Ser	Asn		
	210					215					220						
gca	gtt	gtt	ctg	gcc	gtg	aaa	gaa	gtt	gag	acc	tta	ctt	gca	tct	ata	720	
Ala	Val	Val	Leu	Ala	Val	Lys	Glu	Val	Glu	Thr	Leu	Leu	Ala	Ser	Ile		
225					230				235						240		
gat	gaa	ctt	gct	acc	aaa	gct	att	ggt	aag	aaa	ata	ggc	aat	aat	ggt	768	
Asp	Glu	Leu	Ala	Thr	Lys	Ala	Ile	Gly	Lys	Lys	Ile	Gly	Asn	Asn	Gly		
			245					250					255				
tta	gag	gcc	aat	cag	agt	aaa	aac	aca	tca	ttg	tta	tca	gga	gct	tat	816	
Leu	Glu	Ala	Asn	Gln	Ser	Lys	Asn	Thr	Ser	Leu	Leu	Ser	Gly	Ala	Tyr		
			260					265					270				
gca	ata	tct	gac	cta	ata	gca	gaa	aaa	tta	aat	gta	ttg	aaa	aat	gaa	864	
Ala	Ile	Ser	Asp	Leu	Ile	Ala	Glu	Lys	Leu	Asn	Val	Leu	Lys	Asn	Glu		
		275					280					285					
gaa	tta	aag	gaa	aag	att	gat	aca	gct	aag	caa	tgt	tct	aca	gaa	ttt	912	
Glu	Leu	Lys	Glu	Lys	Ile	Asp	Thr	Ala	Lys	Gln	Cys	Ser	Thr	Glu	Phe		
	290					295					300						
act	aat	aaa	cta	aaa	agt	gaa	cat	gca	gtg	ctt	ggt	ctg	gac	aat	ctt	960	
Thr	Asn	Lys	Leu	Lys	Ser	Glu	His	Ala	Val	Leu	Gly	Leu	Asp	Asn	Leu		
305					310					315					320		

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```

act gat gat aat gca caa aga gct att tta aaa aaa cat gca aat aaa 1008
Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys
          325          330          335

gat aag ggt gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac 1056
Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn
          340          345          350

tta tca aaa gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt 1104
Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu
          355          360          365

aca agt cc 1112
Thr Ser
          370

```

```

<210> 32
<211> 370
<212> PRT
<213> Artificial Sequence

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<220>
<223> OspC Chimera

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```

<400> 32
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
 1          5          10          15
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 20          25          30
Ile Thr Asp Ser Asn Ala Val Leu Ala Val Lys Glu Val Glu Ala
 35          40          45
Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile
 50          55          60
Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu
 65          70          75          80
Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser
 85          90          95
Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Lys
 100          105          110
Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln
 115          120          125
Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu
 130          135          140
Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys
 145          150          155          160
Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu
 165          170          175
Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn
 180          185          190
Ser Arg Lys Asp Gly Asn Ala Ser Thr Asn Ser Ala Asp Glu Ser Val
 195          200          205
Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn
 210          215          220
Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile
 225          230          235          240

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```

Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly
      245      250      255
Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr
      260      265      270
Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu
      275      280      285
Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe
      290      295      300
Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu
      305      310      315
Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys
      325      330      335
Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn
      340      345      350
Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu
      355      360      365
Thr Ser
      370

```

```

<210> 33
<211> 1113
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> OspC Chimera

```

```

<221> CDS
<222> (1)...(1113)

```

```

<400> 33
atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
  1          5          10          15

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
      20          25          30

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
      35          40          45

ttg ctg tca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata 192
Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile
      50          55          60

aaa aac gat ggt agt tta gat aat gaa gca aat cgc aac gag tca ttg 240
Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu
      65          70          75          80

tta gca gga gct tat aca ata tca acc tta ata aca caa aaa tta agt 288
Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser
      85          90          95

aaa tta aac gga tca gaa ggt tta aag gaa aag att gcc gca gct aag 336

```


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Lys	Leu	Asn	Gly	Ser	Glu	Gly	Leu	Lys	Glu	Lys	Ile	Ala	Ala	Ala	Lys	
			100					105					110			
aaa	tgc	tct	gaa	gag	ttt	agt	act	aaa	cta	aaa	gat	aat	cat	gca	cag	384
Lys	Cys	Ser	Glu	Glu	Phe	Ser	Thr	Lys	Leu	Lys	Asp	Asn	His	Ala	Gln	
		115					120					125				
ctt	ggt	ata	cag	ggc	gtt	act	gat	gaa	aat	gca	aaa	aaa	gct	att	tta	432
Leu	Gly	Ile	Gln	Gly	Val	Thr	Asp	Glu	Asn	Ala	Lys	Lys	Ala	Ile	Leu	
	130					135					140					
aaa	gca	aat	gca	gcg	ggt	aaa	gat	aag	ggc	gtt	gaa	gaa	ctt	gaa	aag	480
Lys	Ala	Asn	Ala	Ala	Gly	Lys	Asp	Lys	Gly	Val	Glu	Glu	Leu	Glu	Lys	
145					150				155						160	
ttg	tcc	gga	tca	tta	gaa	agc	tta	tca	aaa	gca	gct	aaa	gag	atg	ctt	528
Leu	Ser	Gly	Ser	Leu	Glu	Ser	Leu	Ser	Lys	Ala	Ala	Lys	Glu	Met	Leu	
				165					170					175		
gct	aat	tca	gtt	aaa	gag	ctt	aca	agc	cct	gtt	gtc	cat	ggt	aat	aat	576
Ala	Asn	Ser	Val	Lys	Glu	Leu	Thr	Ser	Pro	Val	Val	His	Gly	Asn	Asn	
			180					185					190			
tca	ggg	aaa	gat	ggg	aat	aca	tct	gca	aat	tct	gct	gat	gag	tct	gtt	624
Ser	Gly	Lys	Asp	Gly	Asn	Thr	Ser	Ala	Asn	Ser	Ala	Asp	Glu	Ser	Val	
		195					200					205				
aaa	ggg	cct	aat	ctt	aca	gaa	ata	agt	aaa	aaa	att	aca	gaa	tct	aac	672
Lys	Gly	Pro	Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Glu	Ser	Asn	
	210					215					220					
gca	gtt	gtt	ctc	gcc	gtg	aaa	gaa	gtt	gaa	act	ttg	ctt	aca	tct	ata	720
Ala	Val	Val	Leu	Ala	Val	Lys	Glu	Val	Glu	Thr	Leu	Leu	Thr	Ser	Ile	
225					230					235					240	
gat	gag	ctt	gct	aaa	gct	att	ggt	aaa	aaa	ata	aaa	aac	gat	gtt	agt	768
Asp	Glu	Leu	Ala	Lys	Ala	Ile	Gly	Lys	Lys	Ile	Lys	Asn	Asp	Val	Ser	
				245				250						255		
tta	gat	aat	gag	gca	gat	cac	aac	gga	tca	tta	ata	tca	gga	gca	tat	816
Leu	Asp	Asn	Glu	Ala	Asp	His	Asn	Gly	Ser	Leu	Ile	Ser	Gly	Ala	Tyr	
			260					265					270			
tta	att	tca	aac	tta	ata	aca	aaa	aaa	ata	agt	gca	ata	aaa	gat	tca	864
Leu	Ile	Ser	Asn	Leu	Ile	Thr	Lys	Lys	Ile	Ser	Ala	Ile	Lys	Asp	Ser	
		275					280					285				
gga	gaa	ttg	aag	gca	gaa	att	gaa	aag	gct	aag	aaa	tgt	tct	gaa	gaa	912
Gly	Glu	Leu	Lys	Ala	Glu	Ile	Glu	Lys	Ala	Lys	Lys	Cys	Ser	Glu	Glu	
	290					295					300					
ttt	act	gct	aaa	tta	aaa	ggt	gaa	cac	aca	gat	ctt	ggt	aaa	gaa	ggc	960
Phe	Thr	Ala	Lys	Leu	Lys	Gly	Glu	His	Thr	Asp	Leu	Gly	Lys	Glu	Gly	
305					310					315					320	

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```

gtt act gat gat aat gca aaa aaa gcc att tta aaa aca aat aat gat 1008
Val Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp
          325          330          335

aaa act aag ggc gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa 1056
Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys
          340          345          350

aac ttg tca aaa gca gct aaa gag atg ctt act aat tca gtt aaa gag 1104
Asn Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu
          355          360          365

ctt aca agc
Leu Thr Ser
    370

```

```

<210> 34
<211> 371
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> OspC Chimera

```

```

<400> 34
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
 1          5          10          15
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
          20          25          30
Ile Thr Asp Ser Asn Ala Val Leu Ala Val Lys Glu Val Glu Ala
          35          40          45
Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile
          50          55          60
Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu
          65          70          75          80
Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser
          85          90          95
Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Lys
          100          105          110
Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln
          115          120          125
Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu
          130          135          140
Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys
          145          150          155          160
Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu
          165          170          175
Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn
          180          185          190
Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val
          195          200          205
Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn
          210          215          220
Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile
          225          230          235          240

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```

Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser
      245      250      255
Leu Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr
      260      265      270
Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser
      275      280      285
Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu
      290      295      300
Phe Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly
305      310      315      320
Val Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp
      325      330      335
Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys
      340      345      350
Asn Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu
      355      360      365
Leu Thr Ser
      370

```

```

<210> 35
<211> 1112
<212> DNA
<213> Artificial Sequence

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```

<220>
<223> OspC Chimera

```

```

<221> CDS
<222> (1)...(1112)

```

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<400> 35
atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
 1          5          10          15

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
      20          25          30

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
      35          40          45

ttg ctg tca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata 192
Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile
      50          55          60

aaa aac gat ggt agt tta gat aat gaa gca aat cgc aac gag tca ttg 240
Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu
      65          70          75          80

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tta gca gga gct tat aca ata tca acc tta ata aca caa aaa tta agt	288
Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser	
85 90 95	
aaa tta aac gga tca gaa ggt tta aag gaa aag att gcc gca gct aag	336
Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys	
100 105 110	
aaa tgc tct gaa gag ttt agt act aaa cta aaa gat aat cat gca cag	384
Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln	
115 120 125	
ctt ggt ata cag ggc gtt act gat gaa aat gca aaa aaa gct att tta	432
Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu	
130 135 140	
aaa gca aat gca gcg ggt aaa gat aag ggc gtt gaa gaa ctt gaa aag	480
Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys	
145 150 155 160	
ttg tcc gga tca tta gaa agc tta tca aaa gca gct aaa gag atg ctt	528
Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu	
165 170 175	
gct aat tca gtt aaa gag ctt aca agc cct gtt gtc cat ggt aat aat	576
Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn	
180 185 190	
tca gga aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt	624
Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val	
195 200 205	
aaa ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac	672
Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn	
210 215 220	
gca gtt gtt ctg gct gtg aaa gaa att gaa act ttg ctt gca tct ata	720
Ala Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile	
225 230 235 240	
gat gaa ctt gct act aaa gct att ggt aaa aaa ata caa caa aat ggt	768
Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly	
245 250 255	
ggt tta gct gtc gaa gcg ggg cat aat gga aca ttg tta gca ggt gct	816
Gly Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala	
260 265 270	
tat aca ata tca aaa cta ata aca caa aaa tta gat gga ttg aaa aat	864
Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn	
275 280 285	
tca gaa aaa tta aag gaa aaa att gaa aat gct aag aaa tgt tct gaa	912
Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu	
290 295 300	

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```

gat ttt act aaa aaa cta gaa gga gaa cat gcg caa ctt gga att gaa 960
Asp Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu
305          310          315          320

aat gtt act gat gag aat gca aaa aaa gct att tta ata aca gat gca 1008
Asn Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala
          325          330          335

gct aaa gat aag ggc gct gca gag ctt gaa aag cta ttt aaa gca gta 1056
Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val
          340          345          350

gaa aac ttg gca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa 1104
Glu Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys
          355          360          365

gag ctt ac 1112
Glu Leu
370

<210> 36
<211> 370
<212> PRT
<213> Artificial Sequence

<220>
<223> OspC Chimera

<400> 36
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
1          5          10          15
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
          20          25          30

Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
          35          40          45
Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile
50          55          60
Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu
65          70          75          80
Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser
85          90          95
Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys
100          105          110
Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln
115          120          125
Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu
130          135          140
Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys
145          150          155          160
Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu
165          170          175
Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn
180          185          190
Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val
195          200          205

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Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn
 210 215 220
 Ala Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile
 225 230 235 240
 Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly
 245 250 255
 Gly Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala
 260 265 270
 Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn
 275 280 285
 Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu
 290 295 300
 Asp Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu
 305 310 315 320
 Asn Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala
 325 330 335
 Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val
 340 345 350
 Glu Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys
 355 360 365
 Glu Leu
 370

<210> 37
 <211> 1106
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> OspC Chimera

<221> CDS
 <222> (1)...(1106)

<400> 37
 atg gct tgt aat aat tca gga aaa gat ggg aat gca tct gca aat tct 48
 Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser
 1 5 10 15

 gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 20 25 30

 att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa gtt gag acc 144
 Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr
 35 40 45

 tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aaa aaa 192
 Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys
 50 55 60

 ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca ttg 240
 Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu
 65 70 75 80

 tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta aat 288

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Leu	Ser	Gly	Ala	Tyr	Ala	Ile	Ser	Asp	Leu	Ile	Ala	Glu	Lys	Leu	Asn	
				85					90					95		
gta	ttg	aaa	aat	gaa	gaa	tta	aag	gaa	aag	att	gat	aca	gct	aag	caa	336
Val	Leu	Lys	Asn	Glu	Glu	Leu	Lys	Glu	Lys	Ile	Asp	Thr	Ala	Lys	Gln	
			100					105					110			
tgt	tct	aca	gaa	ttt	act	aat	aaa	cta	aaa	agt	gaa	cat	gca	gtg	ctt	384
Cys	Ser	Thr	Glu	Phe	Thr	Asn	Lys	Leu	Lys	Ser	Glu	His	Ala	Val	Leu	
		115					120					125				
ggg	ctg	gac	aat	ctt	act	gat	gat	aat	gca	caa	aga	gct	att	tta	aaa	432
Gly	Leu	Asp	Asn	Leu	Thr	Asp	Asp	Asn	Ala	Gln	Arg	Ala	Ile	Leu	Lys	
	130					135					140					
aaa	cat	gca	aat	aaa	gat	aag	ggg	gct	gca	gaa	ctt	gaa	aag	tta	ttt	480
Lys	His	Ala	Asn	Lys	Asp	Lys	Gly	Ala	Ala	Glu	Leu	Glu	Lys	Leu	Phe	
145					150					155					160	
aaa	gcg	gta	gaa	aac	tta	tca	aaa	gca	gct	caa	gac	aca	tta	aaa	aat	528
Lys	Ala	Val	Glu	Asn	Leu	Ser	Lys	Ala	Ala	Gln	Asp	Thr	Leu	Lys	Asn	
				165				170						175		
gct	gtt	aaa	gag	ctt	aca	agt	cct	att	gtc	cat	ggg	aat	aat	tca	aga	576
Ala	Val	Lys	Glu	Leu	Thr	Ser	Pro	Ile	Val	His	Gly	Asn	Asn	Ser	Arg	
			180					185					190			
aaa	gat	ggg	aat	gca	tct	aca	aat	tct	gcc	gat	gag	tct	gtt	aaa	ggg	624
Lys	Asp	Gly	Asn	Ala	Ser	Thr	Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys	Gly	
		195					200					205				
cct	aat	ctt	aca	gaa	ata	agt	aaa	aaa	att	aca	gaa	tct	aac	gca	gtt	672
Pro	Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Glu	Ser	Asn	Ala	Val	
	210					215					220					
gtt	ctg	gcc	gtg	aaa	gaa	gtt	gag	acc	tta	ctt	gca	tct	ata	gat	gaa	720
Val	Leu	Ala	Val	Lys	Glu	Val	Glu	Thr	Leu	Leu	Ala	Ser	Ile	Asp	Glu	
225					230					235					240	
ctt	gct	acc	aaa	gct	att	ggg	aag	aaa	ata	ggc	aat	aat	ggg	tta	gag	768
Leu	Ala	Thr	Lys	Ala	Ile	Gly	Lys	Lys	Ile	Gly	Asn	Asn	Gly	Leu	Glu	
				245					250					255		
gcc	aat	cag	agt	aaa	aac	aca	tca	ttg	tta	tca	gga	gct	tat	gca	ata	816
Ala	Asn	Gln	Ser	Lys	Asn	Thr	Ser	Leu	Leu	Ser	Gly	Ala	Tyr	Ala	Ile	
			260					265					270			
tct	gac	cta	ata	gca	gaa	aaa	tta	aat	gta	ttg	aaa	aat	gaa	gaa	tta	864
Ser	Asp	Leu	Ile	Ala	Glu	Lys	Leu	Asn	Val	Leu	Lys	Asn	Glu	Glu	Leu	
		275					280					285				
aag	gaa	aag	att	gat	aca	gct	aag	caa	tgt	tct	aca	gaa	ttt	act	aat	912
Lys	Glu	Lys	Ile	Asp	Thr	Ala	Lys	Gln	Cys	Ser	Thr	Glu	Phe	Thr	Asn	
	290					295					300					

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aaa cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat 960
Lys Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp
305 310 315 320

gat aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag 1008
Asp Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys
325 330 335

ggt gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca 1056
Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser
340 345 350

aaa gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt 1104
Lys Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser
355 360 365

cc 1106

<210> 38
<211> 368
<212> PRT
<213> Artificial Sequence

<220>
<223> OspC Chimera

<400> 38
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser
1 5 10 15
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
20 25 30
Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr
35 40 45
Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys
50 55 60
Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu
65 70 75 80
Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn
85 90 95
Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln
100 105 110
Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu
115 120 125
Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys
130 135 140
Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe
145 150 155 160
Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn
165 170 175

Ala Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Arg
180 185 190
Lys Asp Gly Asn Ala Ser Thr Asn Ser Ala Asp Glu Ser Val Lys Gly
195 200 205
Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val
210 215 220

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```

Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu
225          230          235          240
Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu
          245          250          255
Ala Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile
          260          265          270
Ser Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu
          275          280          285
Lys Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn
          290          295          300
Lys Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp
305          310          315          320
Asp Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys
          325          330          335
Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser
          340          345          350
Lys Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser
          355          360          365

```

<210> 39
 <211> 1107
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> OspC Chimera

<221> CDS
 <222> (1)...(1107)

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<400> 39
atg gct tgt aat aat tca gga aaa gat ggg aat gca tct gca aat tct   48
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser
  1          5          10          15

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa   96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
          20          25          30

att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa gtt gag acc   144
Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr
          35          40          45

tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aaa aaa   192
Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys
          50          55          60

ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca ttg   240
Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu
          65          70          75          80

tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta aat   288
Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn
          85          90          95

gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag caa   336

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Val	Leu	Lys	Asn	Glu	Glu	Leu	Lys	Glu	Lys	Ile	Asp	Thr	Ala	Lys	Gln		
			100					105					110				
tgt	tct	aca	gaa	ttt	act	aat	aaa	cta	aaa	agt	gaa	cat	gca	gtg	ctt	384	
Cys	Ser	Thr	Glu	Phe	Thr	Asn	Lys	Leu	Lys	Ser	Glu	His	Ala	Val	Leu		
		115					120					125					
ggc	ctg	gac	aat	ctt	act	gat	gat	aat	gca	caa	aga	gct	att	tta	aaa	432	
Gly	Leu	Asp	Asn	Leu	Thr	Asp	Asp	Asn	Ala	Gln	Arg	Ala	Ile	Leu	Lys		
	130					135					140						
aaa	cat	gca	aat	aaa	gat	aag	ggc	gct	gca	gaa	ctt	gaa	aag	tta	ttt	480	
Lys	His	Ala	Asn	Lys	Asp	Lys	Gly	Ala	Ala	Glu	Leu	Glu	Lys	Leu	Phe		
145					150					155					160		
aaa	gcg	gta	gaa	aac	tta	tca	aaa	gca	gct	caa	gac	aca	tta	aaa	aat	528	
Lys	Ala	Val	Glu	Asn	Leu	Ser	Lys	Ala	Ala	Gln	Asp	Thr	Leu	Lys	Asn		
			165					170						175			
gct	gtt	aaa	gag	ctt	aca	agt	cct	att	gtc	cat	ggc	aat	aat	tca	ggg	576	
Ala	Val	Lys	Glu	Leu	Thr	Ser	Pro	Ile	Val	His	Gly	Asn	Asn	Ser	Gly		
			180					185					190				
aaa	gat	ggg	aat	aca	tct	gca	aat	tct	gct	gat	gag	tct	gtt	aaa	ggg	624	
Lys	Asp	Gly	Asn	Thr	Ser	Ala	Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys	Gly		
		195					200					205					
cct	aat	ctt	aca	gaa	ata	agt	aaa	aaa	att	aca	gaa	tct	aac	gca	gtt	672	
Pro	Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Glu	Ser	Asn	Ala	Val		
		210				215					220						
gtt	ctc	gcc	gtg	aaa	gaa	gtt	gaa	act	ttg	ctt	aca	tct	ata	gat	gag	720	
Val	Leu	Ala	Val	Lys	Glu	Val	Glu	Thr	Leu	Leu	Thr	Ser	Ile	Asp	Glu		
225					230					235					240		
ctt	gct	aaa	gct	att	ggc	aaa	aaa	ata	aaa	aac	gat	gtt	agt	tta	gat	768	
Leu	Ala	Lys	Ala	Ile	Gly	Lys	Lys	Ile	Lys	Asn	Asp	Val	Ser	Leu	Asp		
				245				250						255			
aat	gag	gca	gat	cac	aac	gga	tca	tta	ata	tca	gga	gca	tat	tta	att	816	
Asn	Glu	Ala	Asp	His	Asn	Gly	Ser	Leu	Ile	Ser	Gly	Ala	Tyr	Leu	Ile		
			260					265					270				
tca	aac	tta	ata	aca	aaa	aaa	ata	agt	gca	ata	aaa	gat	tca	gga	gaa	864	
Ser	Asn	Leu	Ile	Thr	Lys	Lys	Ile	Ser	Ala	Ile	Lys	Asp	Ser	Gly	Glu		
		275					280					285					
ttg	aag	gca	gaa	att	gaa	aag	gct	aag	aaa	tgt	tct	gaa	gaa	ttt	act	912	
Leu	Lys	Ala	Glu	Ile	Glu	Lys	Ala	Lys	Lys	Cys	Ser	Glu	Glu	Phe	Thr		
	290					295					300						
gct	aaa	tta	aaa	ggc	gaa	cac	aca	gat	ctt	ggc	aaa	gaa	ggc	gtt	act	960	
Ala	Lys	Leu	Lys	Gly	Glu	His	Thr	Asp	Leu	Gly	Lys	Glu	Gly	Val	Thr		
305					310					315					320		

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gat gat aat gca aaa aaa gcc att tta aaa aca aat aat gat aaa act 1008
 Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr
 325 330 335

aag ggc gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac ttg 1056
 Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu
 340 345 350

tca aaa gca gct aaa gag atg ctt act aat tca gtt aaa gag ctt aca 1104
 Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr
 355 360 365

agc 1107
 Ser

<210> 40
 <211> 369
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> OspC Chimera

<400> 40
 Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser
 1 5 10 15
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 20 25 30
 Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr
 35 40 45
 Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys
 50 55 60
 Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu
 65 70 75 80
 Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn
 85 90 95
 Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln
 100 105 110
 Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu
 115 120 125
 Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys
 130 135 140
 Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe
 145 150 155 160
 Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn
 165 170 175
 Ala Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Gly
 180 185 190
 Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly
 195 200 205
 Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val
 210 215 220
 Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu
 225 230 235 240

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Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp
 245 250 255
 Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile
 260 265 270
 Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu
 275 280 285
 Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr
 290 295 300
 Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr
 305 310 315 320

 Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr
 325 330 335
 Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu
 340 345 350
 Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr
 355 360 365
 Ser

<210> 41
 <211> 1106
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> OspC Chimera

<221> CDS
 <222> (1)...(1106)

<400> 41
 atg gct tgt aat aat tca gga aaa gat ggg aat gca tct gca aat tct 48
 Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser
 1 5 10 15

 gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 20 25 30

 att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa gtt gag acc 144
 Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr
 35 40 45

 tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aaa aaa 192
 Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys
 50 55 60

 ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca ttg 240
 Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu
 65 70 75 80

 tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta aat 288
 Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn
 85 90 95

 gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag caa 336

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Val	Leu	Lys	Asn	Glu	Glu	Leu	Lys	Glu	Lys	Ile	Asp	Thr	Ala	Lys	Gln		
			100					105					110				
tgt	tct	aca	gaa	ttt	act	aat	aaa	cta	aaa	agt	gaa	cat	gca	gtg	ctt	384	
Cys	Ser	Thr	Glu	Phe	Thr	Asn	Lys	Leu	Lys	Ser	Glu	His	Ala	Val	Leu		
		115					120					125					
ggg	ctg	gac	aat	ctt	act	gat	gat	aat	gca	caa	aga	gct	att	tta	aaa	432	
Gly	Leu	Asp	Asn	Leu	Thr	Asp	Asp	Asn	Ala	Gln	Arg	Ala	Ile	Leu	Lys		
	130					135					140						
aaa	cat	gca	aat	aaa	gat	aag	ggg	gct	gca	gaa	ctt	gaa	aag	tta	ttt	480	
Lys	His	Ala	Asn	Lys	Asp	Lys	Gly	Ala	Ala	Glu	Leu	Glu	Lys	Leu	Phe		
145					150					155					160		
aaa	gcg	gta	gaa	aac	tta	tca	aaa	gca	gct	caa	gac	aca	tta	aaa	aat	528	
Lys	Ala	Val	Glu	Asn	Leu	Ser	Lys	Ala	Ala	Gln	Asp	Thr	Leu	Lys	Asn		
			165					170						175			
gct	gtt	aaa	gag	ctt	aca	agt	cct	att	gtc	cat	ggg	aat	aat	tca	gga	576	
Ala	Val	Lys	Glu	Leu	Thr	Ser	Pro	Ile	Val	His	Gly	Asn	Asn	Ser	Gly		
			180					185					190				
aaa	gat	ggg	aat	aca	tct	gca	aat	tct	gct	gat	gag	tct	gtt	aaa	ggg	624	
Lys	Asp	Gly	Asn	Thr	Ser	Ala	Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys	Gly		
		195					200					205					
cct	aat	ctt	aca	gaa	ata	agt	aaa	aaa	att	aca	gaa	tct	aac	gca	gtt	672	
Pro	Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Glu	Ser	Asn	Ala	Val		
		210				215					220						
gtt	ctg	gct	gtg	aaa	gaa	att	gaa	act	ttg	ctt	gca	tct	ata	gat	gaa	720	
Val	Leu	Ala	Val	Lys	Glu	Ile	Glu	Thr	Leu	Leu	Ala	Ser	Ile	Asp	Glu		
225					230				235					240			
ctt	gct	act	aaa	gct	att	ggg	aaa	aaa	ata	caa	caa	aat	ggg	ggg	tta	768	
Leu	Ala	Thr	Lys	Ala	Ile	Gly	Lys	Lys	Ile	Gln	Gln	Asn	Gly	Gly	Leu		
			245						250					255			
gct	gtc	gaa	gcg	ggg	cat	aat	gga	aca	ttg	tta	gca	ggg	gct	tat	aca	816	
Ala	Val	Glu	Ala	Gly	His	Asn	Gly	Thr	Leu	Leu	Ala	Gly	Ala	Tyr	Thr		
			260					265					270				
ata	tca	aaa	cta	ata	aca	caa	aaa	tta	gat	gga	ttg	aaa	aat	tca	gaa	864	
Ile	Ser	Lys	Leu	Ile	Thr	Gln	Lys	Leu	Asp	Gly	Leu	Lys	Asn	Ser	Glu		
		275					280					285					
aaa	tta	aag	gaa	aaa	att	gaa	aat	gct	aag	aaa	tgt	tct	gaa	gat	ttt	912	
Lys	Leu	Lys	Glu	Lys	Ile	Glu	Asn	Ala	Lys	Lys	Cys	Ser	Glu	Asp	Phe		
	290					295					300						
act	aaa	aaa	cta	gaa	gga	gaa	cat	gcg	caa	ctt	gga	att	gaa	aat	gtt	960	
Thr	Lys	Lys	Leu	Glu	Gly	Glu	His	Ala	Gln	Leu	Gly	Ile	Glu	Asn	Val		
305					310					315					320		
act	gat	gag	aat	gca	aaa	aaa	gct	att	tta	ata	aca	gat	gca	gct	aaa	1008	

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Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys
      325                      330                      335

gat aag ggc gct gca gag ctt gaa aag cta ttt aaa gca gta gaa aac 1056
Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn
      340                      345                      350

ttg gca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt 1104
Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu
      355                      360                      365

ac 1106

<210> 42
<211> 368
<212> PRT
<213> Artificial Sequence

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<220>
<223> OspC Chimera

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<400> 42
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser
 1      5      10      15
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 20      25      30
Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr
 35      40      45
Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys
 50      55      60
Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu
 65      70      75      80
Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn
 85      90      95
Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln
 100     105     110
Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu
 115     120     125
Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys
 130     135     140
Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe
 145     150     155     160
Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn
 165     170     175
Ala Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Gly
 180     185     190
Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly
 195     200     205
Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val
 210     215     220
Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu
 225     230     235     240
Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu
 245     250     255

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Ala	Val	Glu	Ala	Gly	His	Asn	Gly	Thr	Leu	Leu	Ala	Gly	Ala	Tyr	Thr		
			260					265					270				
Ile	Ser	Lys	Leu	Ile	Thr	Gln	Lys	Leu	Asp	Gly	Leu	Lys	Asn	Ser	Glu		
		275					280					285					
Lys	Leu	Lys	Glu	Lys	Ile	Glu	Asn	Ala	Lys	Lys	Cys	Ser	Glu	Asp	Phe		
	290					295					300						
Thr	Lys	Lys	Leu	Glu	Gly	Glu	His	Ala	Gln	Leu	Gly	Ile	Glu	Asn	Val		
305					310					315					320		
Thr	Asp	Glu	Asn	Ala	Lys	Lys	Ala	Ile	Leu	Ile	Thr	Asp	Ala	Ala	Lys		
			325					330						335			
Asp	Lys	Gly	Ala	Ala	Glu	Leu	Glu	Lys	Leu	Phe	Lys	Ala	Val	Glu	Asn		
		340					345					350					
Leu	Ala	Lys	Ala	Ala	Lys	Glu	Met	Leu	Ala	Asn	Ser	Val	Lys	Glu	Leu		
		355				360						365					

<210> 43

<211> 633

<212> DNA

<213> *Borrelia burgdorferi*

<220>

<221> CDS

<222> (1)...(633)

<400> 43

atg	aaa	aag	aat	aca	tta	agt	gcg	ata	tta	atg	act	tta	ttt	tta	ttt		48
Met	Lys	Lys	Asn	Thr	Leu	Ser	Ala	Ile	Leu	Met	Thr	Leu	Phe	Leu	Phe		
1				5				10					15				
ata	tct	tgt	aat	aat	tca	ggg	aaa	gat	ggg	aat	aca	tct	gca	aat	tct		96
Ile	Ser	Cys	Asn	Asn	Ser	Gly	Lys	Asp	Gly	Asn	Thr	Ser	Ala	Asn	Ser		
			20					25					30				
gct	gat	gag	tct	gtt	aaa	ggg	cct	aat	ctt	aca	gaa	ata	aat	aaa	aaa		144
Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro	Asn	Leu	Thr	Glu	Ile	Asn	Lys	Lys		
		35				40					45						
att	acg	gat	tct	aat	gcg	gtt	tta	ctt	gct	gtg	aaa	gag	gtt	gaa	gcg		192
Ile	Thr	Asp	Ser	Asn	Ala	Val	Leu	Leu	Ala	Val	Lys	Glu	Val	Glu	Ala		
	50				55						60						
ttg	ctg	tca	tct	ata	gat	gaa	att	gct	gct	aaa	gct	att	ggg	aaa	aaa		240
Leu	Leu	Ser	Ser	Ile	Asp	Glu	Ile	Ala	Ala	Lys	Ala	Ile	Gly	Lys	Lys		
65				70				75						80			
ata	cac	caa	aat	aat	ggg	ttg	gat	acc	gaa	aat	aat	cac	aat	gga	tca		288
Ile	His	Gln	Asn	Asn	Gly	Leu	Asp	Thr	Glu	Asn	Asn	His	Asn	Gly	Ser		
			85					90						95			
ttg	tta	gcg	gga	gct	tat	gca	ata	tca	acc	cta	ata	aaa	caa	aaa	tta		336
Leu	Leu	Ala	Gly	Ala	Tyr	Ala	Ile	Ser	Thr	Leu	Ile	Lys	Gln	Lys	Leu		
		100					105						110				

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gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag	384
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys	
115 120 125	
aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat	432
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp	
130 135 140	
ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta	480
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu	
145 150 155 160	
aaa gca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta	528
Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu	
165 170 175	
ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct	576
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala	
180 185 190	
aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca aaa	624
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys	
195 200 205	
aaa cct taa	633
Lys Pro *	
210	

<210> 44
 <211> 210
 <212> PRT
 <213> *Borrelia burgdorferi*

<400> 44

Met Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe	
1 5 10 15	
Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser	
20 25 30	
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys	
35 40 45	
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala	
50 55 60	
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys	
65 70 75 80	
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser	
85 90 95	
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu	
100 105 110	
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys	
115 120 125	
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp	
130 135 140	

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Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
145                      150                      155                      160
Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu
                      165                      170                      175
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
                      180                      185                      190
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys
                      195                      200                      205
Lys Pro
210

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<210> 45

<211> 580

<212> DNA

<213> *Borrelia burgdorferi*

<220>

<221> CDS

<222> (1)...(580)

<400> 45

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atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct      48
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
1                      5                      10                      15

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata aat aaa aaa      96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys
                      20                      25                      30

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg      144
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
                      35                      40                      45

ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa      192
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
50                      55                      60

ata cac caa aat aat ggt ttg gat acc gaa aat aat cac aat gga tca      240
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser
65                      70                      75                      80

ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta      288
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
                      85                      90                      95

gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag      336
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
100                      105                      110

aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat      384
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
115                      120                      125

ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta      432
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
130                      135                      140

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aaa gca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta 480
Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu
145                      150                      155                      160

ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct 528
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
                      165                      170                      175

aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca tcc 576
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ser
                      180                      185                      190

atg g 580
Met

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<210> 46
<211> 193
<212> PRT
<213> Borrelia burgdorferi

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<400> 46
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1      5      10
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys
20     25     30
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
35     40     45
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
50     55     60
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser
65     70     75
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
85     90     95
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
100    105    110
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
115    120    125
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
130    135    140

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Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu
145    150    155
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
165    170    175
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ser
180    185    190

Met

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<210> 47
<211> 639
<212> DNA
<213> Borrelia garinii

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<222> (1) ... (639)

cca aaa aaa cct taa 639

Pro Lys Lys Pro *
210

<210> 48
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<212> PRT
<213> *Borrelia garinii*

<400> 48
Met Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe
1 5 10 15
Ile Ser Cys Ser Asn Ser Gly Lys Gly Gly Asp Ser Ala Ser Thr Asn
20 25 30
Pro Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys
35 40 45
Lys Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu
50 55 60
Thr Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln
65 70 75 80
Lys Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly
85 90 95
Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys
100 105 110
Leu Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys
115 120 125
Ala Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His
130 135 140
Ala Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala
145 150 155 160
Ile Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys
165 170 175
Asp Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala
180 185 190
Leu Thr Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser
195 200 205
Pro Lys Lys Pro
210

<210> 49
<211> 624
<212> DNA
<213> *Borrelia afzelii*

<220>
<221> CDS
<222> (1)...(624)

<400> 49
atg aaa aag aat aca tta agt gcg ata tta atg act tta ttt tta ttt 48
Met Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe
1 5 10 15

ata tct tgt aat aat tca ggt ggg gat tct gca tct act aat cct gat 96
Ile Ser Cys Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp
20 25 30

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gag tct gca aaa gga cct aat ctt acc gta ata agc aaa aaa att aca	144
Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr	
35 40 45	
gat tct aat gca ttt tta ctg gct gtg aaa gaa gtt gag gct ttg ctt	192
Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu	
50 55 60	
tca tct ata gat gaa ctt tct aaa gct att ggt aaa aaa ata aaa aat	240
Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn	
65 70 75 80	
gat ggt act tta gat aac gaa gca aat cga aac gaa tca ttg ata gca	288
Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala	
85 90 95	
gga gct tat gaa ata tca aaa cta ata aca caa aaa tta agt gta ttg	336
Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu	
100 105 110	
aat tca gaa gaa tta aag aaa aaa att aaa gag gct aag gat tgt tcc	384
Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser	
115 120 125	
caa aaa ttt act act aag cta aaa gat agt cat gca gag ctt ggt ata	432
Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile	
130 135 140	
caa agc gtt cag gat gat aat gca aaa aaa gct att tta aaa aca cat	480
Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His	
145 150 155 160	
gga act aaa gac aag ggt gct aaa gaa ctt gaa gag tta ttt aaa tca	528
Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser	
165 170 175	
cta gaa agc ttg tca aaa gca gcg caa gca gca tta act aat tca gtt	576
Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val	
180 185 190	
aaa gag ctt aca aat cct gtt gtg gca gaa agt cca aaa aaa cct taa	624
Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys Lys Pro *	
195 200 205	

<210> 50

<211> 207

<212> PRT

<213> Borrelia afzelii

<400> 50

Met Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe	
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20 25 30	

<400> 51																
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Met	Ala	Cys	Asn	Asn	Ser	Gly	Lys	Asp	Gly	Asn	Thr	Ser	Ala	Asn	Ser	
1				5					10					15		
gct	gat	gag	tct	gtt	aaa	ggg	cct	aat	ctt	aca	gaa	ata	agt	aaa	aaa	96
Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro	Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	
			20					25					30			
att	acg	gat	tct	aat	gcg	gtt	tta	ctt	gct	gtg	aaa	gag	gtt	gaa	gcg	144
Ile	Thr	Asp	Ser	Asn	Ala	Val	Leu	Leu	Ala	Val	Lys	Glu	Val	Glu	Ala	
		35					40					45				
ttg	ctg	tca	tct	ata	gat	gaa	att	gct	gct	aaa	gct	att	ggg	aaa	aaa	192
Leu	Leu	Ser	Ser	Ile	Asp	Glu	Ile	Ala	Ala	Lys	Ala	Ile	Gly	Lys	Lys	
	50					55					60					
ata	cac	caa	aat	aat	ggg	ttg	gat	acc	gaa	tat	aat	cac	aat	gga	tca	240
Ile	His	Gln	Asn	Asn	Gly	Leu	Asp	Thr	Glu	Tyr	Asn	His	Asn	Gly	Ser	
65					70					75					80	

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ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta	288
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu	
85 90 95	
gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag	336
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys	
100 105 110	
aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat	384
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp	
115 120 125	
ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta	432
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu	
130 135 140	
aaa aca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta	480
Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu	
145 150 155 160	
ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct	528
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala	
165 170 175	
aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca gcc	576
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala	
180 185 190	
atg ggt agt aat tca ggg aaa ggt ggg gat tct gca tct act aat cct	624
Met Gly Ser Asn Ser Gly Lys Gly Gly Asp Ser Ala Ser Thr Asn Pro	
195 200 205	
gct gac gag tct gcg aaa ggg cct aat ctt aca gaa ata agc aaa aaa	672
Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys	
210 215 220	
att aca gat tct aat gca ttt gta ctt gct gtt aaa gaa gtt gag act	720
Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu Thr	
225 230 235 240	
ttg gtt tta tct ata gat gaa ctt gct aag aaa gct att ggt caa aaa	768
Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln Lys	
245 250 255	
ata gac aat aat aat ggt tta gct gct tta aat aat cag aat gga tcg	816
Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly Ser	
260 265 270	
ttg tta gca gga gcc tat gca ata tca acc cta ata aca gaa aaa ttg	864
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys Leu	
275 280 285	
agt aaa ttg aaa aat tta gaa gaa tta aag aca gaa att gca aag gct	912
Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys Ala	
290 295 300	

aag	aaa	tgt	tcc	gaa	gaa	ttt	act	aat	aaa	cta	aaa	agt	ggt	cat	gca	960
Lys	Lys	Cys	Ser	Glu	Glu	Phe	Thr	Asn	Lys	Leu	Lys	Ser	Gly	His	Ala	
305					310					315					320	
gat	ctt	ggc	aaa	cag	gat	gct	acc	gat	gat	cat	gca	aaa	gca	gct	att	1008
Asp	Leu	Gly	Lys	Gln	Asp	Ala	Thr	Asp	Asp	His	Ala	Lys	Ala	Ala	Ile	
				325					330					335		
tta	aaa	aca	cat	gca	act	acc	gat	aaa	ggt	gct	aaa	gaa	ttt	aaa	gat	1056
Leu	Lys	Thr	His	Ala	Thr	Thr	Asp	Lys	Gly	Ala	Lys	Glu	Phe	Lys	Asp	
			340					345					350			
tta	ttt	gaa	tca	gta	gaa	ggt	ttg	tta	aaa	gca	gct	caa	gta	gca	cta	1104
Leu	Phe	Glu	Ser	Val	Glu	Gly	Leu	Leu	Lys	Ala	Ala	Gln	Val	Ala	Leu	
		355					360					365				
act	aat	tca	gtt	aaa	gaa	ctt	ggt	cac	cgt	aat	aat	tca	ggt	ggg	gat	1152
Thr	Asn	Ser	Val	Lys	Glu	Leu	Gly	His	Arg	Asn	Asn	Ser	Gly	Gly	Asp	
	370					375					380					
tct	gca	tct	act	aat	cct	gat	gag	tct	gca	aaa	gga	cct	aat	ctt	acc	1200
Ser	Ala	Ser	Thr	Asn	Pro	Asp	Glu	Ser	Ala	Lys	Gly	Pro	Asn	Leu	Thr	
385					390					395					400	
gta	ata	agc	aaa	aaa	att	aca	gat	tct	aat	gca	ttt	tta	ctg	gct	gtg	1248
Val	Ile	Ser	Lys	Lys	Ile	Thr	Asp	Ser	Asn	Ala	Phe	Leu	Leu	Ala	Val	
				405					410					415		
aaa	gaa	gtt	gag	gct	ttg	ctt	tca	tct	ata	gat	gaa	ctt	tct	aaa	gct	1296
Lys	Glu	Val	Glu	Ala	Leu	Leu	Ser	Ser	Ile	Asp	Glu	Leu	Ser	Lys	Ala	
			420					425					430			
att	ggt	aaa	aaa	ata	aaa	aat	gat	ggt	act	tta	gat	aac	gaa	gca	aat	1344
Ile	Gly	Lys	Lys	Ile	Lys	Asn	Asp	Gly	Thr	Leu	Asp	Asn	Glu	Ala	Asn	
		435					440					445				
cga	aac	gaa	tca	ttg	ata	gca	gga	gct	tat	gaa	ata	tca	aaa	cta	ata	1392
Arg	Asn	Glu	Ser	Leu	Ile	Ala	Gly	Ala	Tyr	Glu	Ile	Ser	Lys	Leu	Ile	
	450					455					460					
aca	caa	aaa	tta	agt	gta	ttg	aat	tca	gaa	gaa	tta	aag	aaa	aaa	att	1440
Thr	Gln	Lys	Leu	Ser	Val	Leu	Asn	Ser	Glu	Glu	Leu	Lys	Lys	Lys	Ile	
465					470					475					480	
aaa	gag	gct	aag	gat	tgt	tcc	caa	aaa	ttt	act	act	aag	cta	aaa	gat	1488
Lys	Glu	Ala	Lys	Asp	Cys	Ser	Gln	Lys	Phe	Thr	Thr	Lys	Leu	Lys	Asp	
				485					490					495		
agt	cat	gca	gag	ctt	ggt	ata	caa	agc	gtt	cag	gat	gat	aat	gca	aaa	1536
Ser	His	Ala	Glu	Leu	Gly	Ile	Gln	Ser	Val	Gln	Asp	Asp	Asn	Ala	Lys	
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<210> 52
<211> 560
<212> PRT
<213> ospC Chimera
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<400>	52														
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Ala	Asp	Glu	Ser 20	Val	Lys	Gly	Pro	Asn 25	Leu	Thr	Glu	Ile	Ser 30	Lys	Lys
Ile	Thr	Asp 35	Ser	Asn	Ala	Val	Leu 40	Leu	Ala	Val	Lys	Glu 45	Val	Glu	Ala
Leu	Leu 50	Ser	Ser	Ile	Asp	Glu 55	Ile	Ala	Ala	Lys	Ala 60	Ile	Gly	Lys	Lys
Ile 65	His	Gln	Asn	Asn 70	Gly	Leu	Asp	Thr	Glu	Tyr 75	Asn	His	Asn	Gly	Ser 80
Leu	Leu	Ala	Gly 85	Ala	Tyr	Ala	Ile	Ser	Thr 90	Leu	Ile	Lys	Gln	Lys 95	Leu
Asp	Gly	Leu	Lys 100	Asn	Glu	Gly	Leu	Lys 105	Glu	Lys	Ile	Asp	Ala 110	Ala	Lys
Lys	Cys	Ser 115	Glu	Thr	Phe	Thr	Asn 120	Lys	Leu	Lys	Glu	Lys 125	His	Thr	Asp
Leu	Gly 130	Lys	Glu	Gly	Val	Thr 135	Asp	Ala	Asp	Ala	Lys 140	Glu	Ala	Ile	Leu
Lys 145	Thr	Asn	Gly	Thr	Lys 150	Thr	Lys	Gly	Ala	Glu 155	Glu	Leu	Gly	Lys 160	Leu
Phe	Glu	Ser	Val 165	Glu	Val	Leu	Ser	Lys	Ala 170	Ala	Lys	Glu	Met 175	Leu	Ala
Asn	Ser	Val 180	Lys	Glu	Leu	Thr	Ser	Pro 185	Val	Val	Ala	Glu	Ser 190	Pro	Ala
Met	Gly 195	Ser	Asn	Ser	Gly	Lys	Gly 200	Asp	Ser	Ala	Ser 205	Thr	Asn	Pro	
Ala	Asp 210	Glu	Ser	Ala	Lys	Gly 215	Pro	Asn	Leu	Thr	Glu 220	Ile	Ser	Lys	Lys
Ile 225	Thr	Asp	Ser	Asn 230	Ala	Phe	Val	Leu	Ala	Val 235	Lys	Glu	Val	Glu	Thr 240
Leu	Val	Leu	Ser 245	Ile	Asp	Glu	Leu	Ala	Lys 250	Lys	Ala	Ile	Gly	Gln 255	Lys
Ile	Asp	Asn 260	Asn	Asn	Gly	Leu	Ala	Ala 265	Leu	Asn	Asn	Gln	Asn 270	Gly	Ser

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Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys Leu
 275 280 285
 Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys Ala
 290 295 300
 Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His Ala
 305 310 315 320
 Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala Ile
 325 330 335
 Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys Asp
 340 345 350
 Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala Leu
 355 360 365
 Thr Asn Ser Val Lys Glu Leu Gly His Arg Asn Asn Ser Gly Gly Asp
 370 375 380
 Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr
 385 390 395 400
 Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val
 405 410 415
 Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala
 420 425 430
 Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn
 435 440 445
 Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile
 450 455 460
 Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile
 465 470 475 480

 Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp
 485 490 495
 Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys
 500 505 510
 Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu
 515 520 525
 Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln
 530 535 540
 Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala
 545 550 555 560

<210> 53
 <211> 1137
 <212> DNA
 <213> ospC Chimera

<220>
 <221> CDS
 <222> (1)...(1137)

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 1 5 10 15

 gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 20 25 30

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att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala 35 40 45	144
ttg ctg tca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile 50 55 60	192
aaa aac gat ggt agt tta gat aat gaa gca aat cgc aac gag tca ttg Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu 65 70 75 80	240
tta gca gga gct tat aca ata tca acc tta ata aca caa aaa tta agt Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser 85 90 95	288
aaa tta aac gga tca gaa ggt tta aag gaa aag att gcc gca gct aag Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys 100 105 110	336
aaa tgc tct gaa gag ttt agt act aaa cta aaa gat aat cat gca cag Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln 115 120 125	384
ctt ggt ata cag ggc gtt act gat gaa aat gca aaa aaa gct att tta Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu 130 135 140	432
aaa gca aat gca gcg ggt aaa gat aag ggc gtt gaa gaa ctt gaa aag Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys 145 150 155 160	480
ttg tcc gga tca tta gaa agc tta tca aaa gca gct aaa gag atg ctt Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu 165 170 175	528
gct aat tca gtt aaa gag ctt aca agc cct gtt gtc cat ggt aat aat Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn 180 185 190	576
tca ggt ggg gat tct gca tct act aat cct gat gag tct gca aaa gga Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly 195 200 205	624
cct aat ctt acc gta ata agc aaa aaa att aca gat tct aat gca ttt Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe 210 215 220	672
tta ctg gct gtg aaa gaa gtt gag gct ttg ctt tca tct ata gat gaa Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu 225 230 235 240	720
ctt tct aaa gct att ggt aaa aaa ata aaa aat gat ggt act tta gat Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp 245 250 255	768

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aac gaa gca aat cga aac gaa tca ttg ata gca gga gct tat gaa ata	816
Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile	
260 265 270	
tca aaa cta ata aca caa aaa tta agt gta ttg aat tca gaa gaa tta	864
Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu	
275 280 285	
aag aaa aaa att aaa gag gct aag gat tgt tcc caa aaa ttt act act	912
Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr	
290 295 300	
aag cta aaa gat agt cat gca gag ctt ggt ata caa agc gtt cag gat	960
Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp	
305 310 315 320	
gat aat gca aaa aaa gct att tta aaa aca cat gga act aaa gac aag	1008
Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys	
325 330 335	
ggt gct aaa gaa ctt gaa gag tta ttt aaa tca cta gaa agc ttg tca	1056
Gly Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser	
340 345 350	
aaa gca gcg caa gca gca tta act aat tca gtt aaa gag ctt aca aat	1104
Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn	
355 360 365	
cct gtt gtg gca gaa agt cca aaa aaa cct taa	1137
Pro Val Val Ala Glu Ser Pro Lys Lys Pro *	
370 375	

<210> 54
 <211> 378
 <212> PRT
 <213> ospC Chimera

<400> 54
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 20 25 30
 Ile Thr Asp Ser Asn Ala Val Leu Ala Val Lys Glu Val Glu Ala
 35 40 45
 Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile
 50 55 60
 Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu
 65 70 75 80
 Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser
 85 90 95
 Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Lys
 100 105 110

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Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln
 115 120 125
 Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu
 130 135 140
 Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys
 145 150 155 160
 Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu
 165 170 175
 Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn
 180 185 190
 Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly
 195 200 205
 Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe
 210 215 220
 Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu
 225 230 235 240
 Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp
 245 250 255
 Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile
 260 265 270
 Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu
 275 280 285
 Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr
 290 295 300
 Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp
 305 310 315 320
 Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys
 325 330 335
 Gly Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser
 340 345 350
 Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn
 355 360 365
 Pro Val Val Ala Glu Ser Pro Lys Lys Pro
 370 375

<210> 55
 <211> 1158
 <212> DNA
 <213> ospC Chimera

<220>
 <221> CDS
 <222> (1)...(1158)

<400> 55
 atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48
 Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
 1 5 10 15
 gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 20 25 30

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att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala 35 40 45	144
ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys 50 55 60	192
ata cac caa aat aat ggt ttg gat acc gaa tat aat cac aat gga tca Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser 65 70 75 80	240
ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu 85 90 95	288
gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys 100 105 110	336
aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp 115 120 125	384
ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu 130 135 140	432
aaa aca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu 145 150 155 160	480
ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala 165 170 175	528
aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca aaa Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys 180 185 190	576
aaa cct ttc cat ggt aat aat tca ggt ggg gat tct gca tct act aat Lys Pro Phe His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn 195 200 205	624
cct gat gag tct gca aaa gga cct aat ctt acc gta ata agc aaa aaa Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys Lys 210 215 220	672
att aca gat tct aat gca ttt tta ctg gct gtg aaa gaa gtt gag gct Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu Ala 225 230 235 240	720
ttg ctt tca tct ata gat gaa ctt tct aaa gct att ggt aaa aaa ata Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile 245 250 255	768

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aaa aat gat ggt act tta gat aac gaa gca aat cga aac gaa tca ttg 816
Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu
260 265 270

ata gca gga gct tat gaa ata tca aaa cta ata aca caa aaa tta agt 864
Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser
275 280 285

gta ttg aat tca gaa gaa tta aag aaa aaa att aaa gag gct aag gat 912
Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp
290 295 300

tgt tcc caa aaa ttt act act aag cta aaa gat agt cat gca gag ctt 960
Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu Leu
305 310 315 320

ggt ata caa agc gtt cag gat gat aat gca aaa aaa gct att tta aaa 1008
Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys
325 330 335

aca cat gga act aaa gac aag ggt gct aaa gaa ctt gaa gag tta ttt 1056
Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu Phe
340 345 350

aaa tca cta gaa agc ttg tca aaa gca gcg caa gca gca tta act aat 1104
Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn
355 360 365

tca gtt aaa gag ctt aca aat cct gtt gtg gca gaa agt cca aaa aaa 1152
Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys Lys
370 375 380

cct taa 1158
Pro *
385

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<210> 56
<211> 385
<212> PRT
<213> ospC Chimera

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<400> 56
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
1 5 10 15
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
20 25 30
Ile Thr Asp Ser Asn Ala Val Leu Ala Val Lys Glu Val Glu Ala
35 40 45

Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
50 55 60
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser
65 70 75 80
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
85 90 95

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Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
 100 105 110
 Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
 115 120 125
 Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
 130 135 140
 Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Leu Gly Lys Leu
 145 150 155 160
 Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
 165 170 175
 Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys
 180 185 190
 Lys Pro Phe His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn
 195 200 205
 Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys Lys
 210 215 220
 Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu Ala
 225 230 235 240
 Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile
 245 250 255
 Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu
 260 265 270
 Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser
 275 280 285
 Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp
 290 295 300
 Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu Leu
 305 310 315 320
 Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys
 325 330 335
 Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu Phe
 340 345 350
 Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn
 355 360 365
 Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys Lys
 370 375 380
 Pro
 385

<210> 57
 <211> 1161
 <212> DNA
 <213> ospC Chimera

<220>
 <221> CDS
 <222> (1)...(1161)

<400> 57
 atg tgt agt aat tca ggg aaa ggt ggg gat tct gca tct act aat cct 48
 Met Cys Ser Asn Ser Gly Lys Gly Gly Asp Ser Ala Ser Thr Asn Pro
 1 5 10 15

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gct gac gag tct gcg aaa ggg cct aat ctt aca gaa ata agc aaa aaa	96
Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys	
20 25 30	
att aca gat tct aat gca ttt gta ctt gct gtt aaa gaa gtt gag act	144
Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu Thr	
35 40 45	
ttg gtt tta tct ata gat gaa ctt gct aag aaa gct att ggt caa aaa	192
Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln Lys	
50 55 60	
ata gac aat aat aat ggt tta gct gct tta aat aat cag aat gga tcg	240
Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly Ser	
65 70 75 80	
ttg tta gca gga gcc tat gca ata tca acc cta ata aca gaa aaa ttg	288
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys Leu	
85 90 95	
agt aaa ttg aaa aat tta gaa gaa tta aag aca gaa att gca aag gct	336
Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys Ala	
100 105 110	
aag aaa tgt tcc gaa gaa ttt act aat aaa cta aaa agt ggt cat gca	384
Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His Ala	
115 120 125	
gat ctt ggc aaa cag gat gct acc gat gat cat gca aaa gca gct att	432
Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala Ile	
130 135 140	
tta aaa aca cat gca act acc gat aaa ggt gct aaa gaa ttt aaa gat	480
Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys Asp	
145 150 155 160	
tta ttt gaa tca gta gaa ggt ttg tta aaa gca gct caa gta gca cta	528
Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala Leu	
165 170 175	
act aat tca gtt aaa gaa ctt aca agt cct gtt gta gca gaa agt cca	576
Thr Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro	
180 185 190	
aaa aaa cct cat atg gct aat aat tca ggt ggg gat tct gca tct act	624
Lys Lys Pro His Met Ala Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr	
195 200 205	
aat cct gat gag tct gca aaa gga cct aat ctt acc gta ata agc aaa	672
Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys	
210 215 220	
aaa att aca gat tct aat gca ttt tta ctg gct gtg aaa gaa gtt gag	720
Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu	
225 230 235 240	

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gct ttg ctt tca tct ata gat gaa ctt tct aaa gct att ggt aaa aaa 768
Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys
245 250 255

ata aaa aat gat ggt act tta gat aac gaa gca aat cga aac gaa tca 816
Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser
260 265 270

ttg ata gca gga gct tat gaa ata tca aaa cta ata aca caa aaa tta 864
Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu
275 280 285

agt gta ttg aat tca gaa gaa tta aag aaa aaa att aaa gag gct aag 912
Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys
290 295 300

gat tgt tcc caa aaa ttt act act aag cta aaa gat agt cat gca gag 960
Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu
305 310 315 320

ctt ggt ata caa agc gtt cag gat gat aat gca aaa aaa gct att tta 1008
Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu
325 330 335

aaa aca cat gga act aaa gac aag ggt gct aaa gaa ctt gaa gag tta 1056
Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu
340 345 350

ttt aaa tca cta gaa agc ttg tca aaa gca gcg caa gca gca tta act 1104
Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr
355 360 365

aat tca gtt aaa gag ctt aca aat cct gtt gtg gca gaa agt cca aaa 1152
Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys
370 375 380

aaa cct taa 1161
Lys Pro *
385

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<210> 58
<211> 386
<212> PRT
<213> ospC Chimera

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<400> 58
Met Cys Ser Asn Ser Gly Lys Gly Gly Asp Ser Ala Ser Thr Asn Pro
1 5 10 15
Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
20 25 30
Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu Thr
35 40 45
Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln Lys
50 55 60

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Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly Ser
65      70      75      80
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys Leu
      85      90      95
Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys Ala
      100      105      110
Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His Ala
      115      120      125
Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala Ile
      130      135      140

Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys Asp
145      150      155      160
Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala Leu
      165      170      175
Thr Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro
      180      185      190
Lys Lys Pro His Met Ala Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr
      195      200      205
Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys
      210      215      220
Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu
225      230      235      240
Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys
      245      250      255
Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser
      260      265      270
Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu
      275      280      285
Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys
      290      295      300
Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu
305      310      315      320
Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu
      325      330      335
Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu
      340      345      350
Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr
      355      360      365
Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys
      370      375      380
Lys Pro
385

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<210> 59
<211> 1197
<212> DNA
<213> ospC Chimera

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<220>
<221> CDS
<222> (1)...(1197)

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<400> 59

atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt	48
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys	
1 5 10 15	
gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa	96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys	
20 25 30	
gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct	144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro	
35 40 45	
aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta	192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu	
50 55 60	
ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att	240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile	
65 70 75 80	
gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat	288
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp	
85 90 95	
acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata	336
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile	
100 105 110	
tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta	384
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu	
115 120 125	
aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat	432
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn	
130 135 140	
aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat	480
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp	
145 150 155 160	
gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa	528
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys	
165 170 175	
ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca	576
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser	
180 185 190	
aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc	624
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser	
195 200 205	

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cct gtt gtg gca gaa agt cca gcc atg gta aat aat tca ggg aaa gat	672
Pro Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp	
210 215 220	
ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat	720
Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn	
225 230 235 240	
ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctc	768
Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu	
245 250 255	
gcc gtg aaa gaa gtt gaa act ttg ctt aca tct ata gat gag ctt gct	816
Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala	
260 265 270	
aaa gct att ggt aaa aaa ata aaa aac gat gtt agt tta gat aat gag	864
Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu	
275 280 285	
gca gat cac aac gga tca tta ata tca gga gca tat tta att tca aac	912
Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn	
290 295 300	
tta ata aca aaa aaa ata agt gca ata aaa gat tca gga gaa ttg aag	960
Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys	
305 310 315 320	
gca gaa att gaa aag gct aag aaa tgt tct gaa gaa ttt act gct aaa	1008
Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys	
325 330 335	
tta aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc gtt act gat gat	1056
Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp	
340 345 350	
aat gca aaa aaa gcc att tta aaa aca aat aat gat aaa act aag ggc	1104
Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly	
355 360 365	
gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac ttg tca aaa	1152
Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys	
370 375 380	
gca gct aaa gag atg ctt act aat tca gtt aaa gag ctt aca agc	1197
Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser	
385 390 395	

<210> 60

<211> 399

<212> PRT

<213> ospC Chimera

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<400> 60

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Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1      5      10      15
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20      25      30
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35      40      45
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
 50      55      60
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile
 65      70      75      80
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp
 85      90      95
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile
 100     105     110
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu
 115     120     125
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn
 130     135     140
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp
 145     150     155     160
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys
 165     170     175
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser
 180     185     190
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
 195     200     205
Pro Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp
 210     215     220
Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
 225     230     235     240

Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu
 245     250     255
Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala
 260     265     270
Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu
 275     280     285
Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn
 290     295     300
Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys
 305     310     315     320
Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys
 325     330     335
Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp
 340     345     350
Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly
 355     360     365
Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys
 370     375     380
Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser
 385     390     395

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<210> 61

<211> 1196

<212> DNA

<213> ospC Chimera

<220>

<221> CDS

<222> (1)...(1196)

<400> 61

atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt	48
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys	
1 5 10 15	
gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa	96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys	
20 25 30	
gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct	144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro	
35 40 45	
aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta	192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu	
50 55 60	
ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att	240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile	
65 70 75 80	
gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat	288
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp	
85 90 95	
acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata	336
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile	
100 105 110	
tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta	384
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu	
115 120 125	
aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat	432
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn	
130 135 140	
aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat	480
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp	
145 150 155 160	
gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa	528
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys	
165 170 175	
ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca	576
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser	
180 185 190	

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aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser 195 200 205	624
cct gtt gtg gca gaa agt cca gcc atg gta aat aat tca gga aaa gat Pro Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp 210 215 220	672
ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn 225 230 235 240	720
ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu 245 250 255	768
gct gtg aaa gaa att gaa act ttg ctt gca tct ata gat gaa ctt gct Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala 260 265 270	816
act aaa gct att ggt aaa aaa ata caa caa aat ggt ggt tta gct gtc Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val 275 280 285	864
gaa gcg ggg cat aat gga aca ttg tta gca ggt gct tat aca ata tca Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser 290 295 300	912
aaa cta ata aca caa aaa tta gat gga ttg aaa aat tca gaa aaa tta Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu 305 310 315 320	960
aag gaa aaa att gaa aat gct aag aaa tgt tct gaa gat ttt act aaa Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys 325 330 335	1008
aaa cta gaa gga gaa cat gcg caa ctt gga att gaa aat gtt act gat Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp 340 345 350	1056
gag aat gca aaa aaa gct att tta ata aca gat gca gct aaa gat aag Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys 355 360 365	1104
ggc gct gca gag ctt gaa aag cta ttt aaa gca gta gaa aac ttg gca Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala 370 375 380	1152
aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt ac Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu 385 390 395	1196

<210> 62
<211> 398

73/108

<212> PRT

<213> ospC Chimera

<400> 62

Met	Arg	Leu	Leu	Ile	Gly	Phe	Ala	Leu	Ala	Leu	Ala	Leu	Ile	Gly	Cys
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Ala	Gln	Lys	Gly	Ala	Glu	Ser	Ile	Gly	Ser	Cys	Asn	Asn	Ser	Gly	Lys
			20					25					30		
Asp	Gly	Asn	Thr	Ser	Ala	Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro
		35					40					45			
Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Asp	Ser	Asn	Ala	Val	Leu
	50					55					60				
Leu	Ala	Val	Lys	Glu	Val	Glu	Ala	Leu	Leu	Ser	Ser	Ile	Asp	Glu	Ile
65					70					75				80	
Ala	Ala	Lys	Ala	Ile	Gly	Lys	Lys	Ile	His	Gln	Asn	Asn	Gly	Leu	Asp
				85					90					95	
Thr	Glu	Tyr	Asn	His	Asn	Gly	Ser	Leu	Leu	Ala	Gly	Ala	Tyr	Ala	Ile
			100					105					110		
Ser	Thr	Leu	Ile	Lys	Gln	Lys	Leu	Asp	Gly	Leu	Lys	Asn	Glu	Gly	Leu
		115					120					125			
Lys	Glu	Lys	Ile	Asp	Ala	Ala	Lys	Lys	Cys	Ser	Glu	Thr	Phe	Thr	Asn
	130					135					140				
Lys	Leu	Lys	Glu	Lys	His	Thr	Asp	Leu	Gly	Lys	Glu	Gly	Val	Thr	Asp
145					150					155					160
Ala	Asp	Ala	Lys	Glu	Ala	Ile	Leu	Lys	Thr	Asn	Gly	Thr	Lys	Thr	Lys
				165					170					175	
Gly	Ala	Glu	Glu	Leu	Gly	Lys	Leu	Phe	Glu	Ser	Val	Glu	Val	Leu	Ser
			180					185					190		
Lys	Ala	Ala	Lys	Glu	Met	Leu	Ala	Asn	Ser	Val	Lys	Glu	Leu	Thr	Ser
		195					200					205			
Pro	Val	Val	Ala	Glu	Ser	Pro	Ala	Met	Val	Asn	Asn	Ser	Gly	Lys	Asp
	210					215					220				
Gly	Asn	Thr	Ser	Ala	Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro	Asn
					230					235					240
Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Glu	Ser	Asn	Ala	Val	Val	Leu
				245					250					255	
Ala	Val	Lys	Glu	Ile	Glu	Thr	Leu	Leu	Ala	Ser	Ile	Asp	Glu	Leu	Ala
			260					265					270		
Thr	Lys	Ala	Ile	Gly	Lys	Lys	Ile	Gln	Gln	Asn	Gly	Gly	Leu	Ala	Val
		275					280					285			
Glu	Ala	Gly	His	Asn	Gly	Thr	Leu	Leu	Ala	Gly	Ala	Tyr	Thr	Ile	Ser
	290					295					300				
Lys	Leu	Ile	Thr	Gln	Lys	Leu	Asp	Gly	Leu	Lys	Asn	Ser	Glu	Lys	Leu
305					310					315					320
Lys	Glu	Lys	Ile	Glu	Asn	Ala	Lys	Lys	Cys	Ser	Glu	Asp	Phe	Thr	Lys
				325					330					335	
Lys	Leu	Glu	Gly	Glu	His	Ala	Gln	Leu	Gly	Ile	Glu	Asn	Val	Thr	Asp
			340					345					350		
Glu	Asn	Ala	Lys	Lys	Ala	Ile	Leu	Ile	Thr	Asp	Ala	Ala	Lys	Asp	Lys
		355					360					365			
Gly	Ala	Ala	Glu	Leu	Glu	Lys	Leu	Phe	Lys	Ala	Val	Glu	Asn	Leu	Ala
	370					375					380				
Lys	Ala	Ala	Lys	Glu	Met	Leu	Ala	Asn	Ser	Val	Lys	Glu	Leu		
385					390					395					

<210> 63
 <211> 1185
 <212> DNA
 <213> ospC Chimera

<220>
 <221> CDS
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 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
 50 55 60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt 240
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu
 65 70 75 80

gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat 288
 Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn
 85 90 95

gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca 336
 Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser
 100 105 110

acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta 384
 Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu
 115 120 125

aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act 432
 Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr
 130 135 140

aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat 480
 Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp
 145 150 155 160

gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat 528
 Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp
 165 170 175

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aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta	576
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu	
180 185 190	
tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca	624
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr	
195 200 205	
agc cct gtt gtc cat ggt aat aat tca ggg aaa gat ggg aat aca tct	672
Ser Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser	
210 215 220	
gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata	720
Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile	
225 230 235 240	
agt aaa aaa att aca gaa tct aac gca gtt gtt ctc gcc gtg aaa gaa	768
Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu	
245 250 255	
gtt gaa act ttg ctt aca tct ata gat gag ctt gct aaa gct att ggt	816
Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly	
260 265 270	
aaa aaa ata aaa aac gat gtt agt tta gat aat gag gca gat cac aac	864
Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn	
275 280 285	
gga tca tta ata tca gga gca tat tta att tca aac tta ata aca aaa	912
Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys	
290 295 300	
aaa ata agt gca ata aaa gat tca gga gaa ttg aag gca gaa att gaa	960
Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu	
305 310 315 320	
aag gct aag aaa tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa	1008
Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu	
325 330 335	
cac aca gat ctt ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa	1056
His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys	
340 345 350	
gcc att tta aaa aca aat aat gat aaa act aag ggc gct gat gaa ctt	1104
Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu	
355 360 365	
gaa aag tta ttt gaa tca gta aaa aac ttg tca aaa gca gct aaa gag	1152
Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu	
370 375 380	
atg ctt act aat tca gtt aaa gag ctt aca agc	1185
Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser	
385 390 395	

<210> 64
 <211> 395
 <212> PRT
 <213> ospC Chimera

<400> 64

Met	Arg	Leu	Leu	Ile	Gly	Phe	Ala	Leu	Ala	Leu	Ala	Leu	Ile	Gly	Cys
1				5					10					15	
Ala	Gln	Lys	Gly	Ala	Glu	Ser	Ile	Gly	Ser	Cys	Asn	Asn	Ser	Gly	Lys
			20					25					30		
Asp	Gly	Asn	Thr	Ser	Ala	Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro
		35					40					45			
Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Asp	Ser	Asn	Ala	Val	Leu
	50					55					60				
Leu	Ala	Val	Lys	Glu	Val	Glu	Ala	Leu	Leu	Ser	Ser	Ile	Asp	Glu	Leu
65					70					75					80
Ala	Lys	Ala	Ile	Gly	Lys	Lys	Ile	Lys	Asn	Asp	Gly	Ser	Leu	Asp	Asn
				85					90					95	
Glu	Ala	Asn	Arg	Asn	Glu	Ser	Leu	Leu	Ala	Gly	Ala	Tyr	Thr	Ile	Ser
			100					105					110		
Thr	Leu	Ile	Thr	Gln	Lys	Leu	Ser	Lys	Leu	Asn	Gly	Ser	Glu	Gly	Leu
		115					120					125			
Lys	Glu	Lys	Ile	Ala	Ala	Ala	Lys	Lys	Cys	Ser	Glu	Glu	Phe	Ser	Thr
	130						135					140			
Lys	Leu	Lys	Asp	Asn	His	Ala	Gln	Leu	Gly	Ile	Gln	Gly	Val	Thr	Asp
145					150					155					160
Glu	Asn	Ala	Lys	Lys	Ala	Ile	Leu	Lys	Ala	Asn	Ala	Ala	Gly	Lys	Asp
				165					170					175	
Lys	Gly	Val	Glu	Glu	Leu	Glu	Lys	Leu	Ser	Gly	Ser	Leu	Glu	Ser	Leu
		180						185					190		
Ser	Lys	Ala	Ala	Lys	Glu	Met	Leu	Ala	Asn	Ser	Val	Lys	Glu	Leu	Thr
		195					200					205			
Ser	Pro	Val	Val	His	Gly	Asn	Asn	Ser	Gly	Lys	Asp	Gly	Asn	Thr	Ser
	210					215					220				
Ala	Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro	Asn	Leu	Thr	Glu	Ile
225					230					235					240
Ser	Lys	Lys	Ile	Thr	Glu	Ser	Asn	Ala	Val	Val	Leu	Ala	Val	Lys	Glu
				245					250					255	
Val	Glu	Thr	Leu	Leu	Thr	Ser	Ile	Asp	Glu	Leu	Ala	Lys	Ala	Ile	Gly
		260						265					270		
Lys	Lys	Ile	Lys	Asn	Asp	Val	Ser	Leu	Asp	Asn	Glu	Ala	Asp	His	Asn
		275					280					285			
Gly	Ser	Leu	Ile	Ser	Gly	Ala	Tyr	Leu	Ile	Ser	Asn	Leu	Ile	Thr	Lys
	290					295					300				
Lys	Ile	Ser	Ala	Ile	Lys	Asp	Ser	Gly	Glu	Leu	Lys	Ala	Glu	Ile	Glu
305					310					315					320
Lys	Ala	Lys	Lys	Cys	Ser	Glu	Glu	Phe	Thr	Ala	Lys	Leu	Lys	Gly	Glu
				325					330					335	
His	Thr	Asp	Leu	Gly	Lys	Glu	Gly	Val	Thr	Asp	Asp	Asn	Ala	Lys	Lys
			340					345					350		
Ala	Ile	Leu	Lys	Thr	Asn	Asn	Asp	Lys	Thr	Lys	Gly	Ala	Asp	Glu	Leu
		355					360					365			
Glu	Lys	Leu	Phe	Glu	Ser	Val	Lys	Asn	Leu	Ser	Lys	Ala	Ala	Lys	Glu
	370					375					380				
Met	Leu	Thr	Asn	Ser	Val	Lys	Glu	Leu	Thr	Ser					
385					390					395					

<210> 65
 <211> 1184
 <212> DNA
 <213> ospC Chimera

<220>
 <221> CDS
 <222> (1)...(1184)

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 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
 50 55 60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt 240
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu
 65 70 75 80

gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat 288
 Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn
 85 90 95

gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca 336
 Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser
 100 105 110

acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta 384
 Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu
 115 120 125

aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act 432
 Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr
 130 135 140

aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat 480
 Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp
 145 150 155 160

gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat 528
 Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp
 165 170 175

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aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta	576
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu	
180 185 190	
tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca	624
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr	
195 200 205	
agc cct gtt gtc cat ggt aat aat tca gga aaa gat ggg aat aca tct	672
Ser Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser	
210 215 220	
gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata	720
Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile	
225 230 235 240	
agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gct gtg aaa gaa	768
Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu	
245 250 255	
att gaa act ttg ctt gca tct ata gat gaa ctt gct act aaa gct att	816
Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile	
260 265 270	
ggt aaa aaa ata caa caa aat ggt ggt tta gct gtc gaa gcg ggg cat	864
Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His	
275 280 285	
aat gga aca ttg tta gca ggt gct tat aca ata tca aaa cta ata aca	912
Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr	
290 295 300	
caa aaa tta gat gga ttg aaa aat tca gaa aaa tta aag gaa aaa att	960
Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile	
305 310 315 320	
gaa aat gct aag aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga	1008
Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly	
325 330 335	
gaa cat gcg caa ctt gga att gaa aat gtt act gat gag aat gca aaa	1056
Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys	
340 345 350	
aaa gct att tta ata aca gat gca gct aaa gat aag ggc gct gca gag	1104
Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu	
355 360 365	
ctt gaa aag cta ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa	1152
Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys	
370 375 380	
gag atg ctt gct aat tca gtt aaa gag ctt ac	1184
Glu Met Leu Ala Asn Ser Val Lys Glu Leu	
385 390	

<400> 66

Met 1	Arg	Leu	Leu	Ile 5	Gly	Phe	Ala	Leu	Ala 10	Leu	Ala	Leu	Ile	Gly 15	Cys
Ala	Gln	Lys	Gly 20	Ala	Glu	Ser	Ile	Gly 25	Ser	Cys	Asn	Asn	Ser 30	Gly	Lys
Asp	Gly	Asn 35	Thr	Ser	Ala	Asn	Ser 40	Ala	Asp	Glu	Ser	Val 45	Lys	Gly	Pro
Asn	Leu 50	Thr	Glu	Ile	Ser	Lys 55	Lys	Ile	Thr	Asp	Ser 60	Asn	Ala	Val	Leu
Leu 65	Ala	Val	Lys	Glu 70	Val	Glu	Ala	Leu	Leu 75	Ser	Ser	Ile	Asp	Glu 80	Leu
Ala	Lys	Ala	Ile 85	Gly	Lys	Lys	Ile	Lys	Asn 90	Asp	Gly	Ser	Leu	Asp 95	Asn
Glu	Ala	Asn 100	Arg	Asn	Glu	Ser	Leu 105	Leu	Ala	Gly	Ala	Tyr 110	Thr	Ile	Ser
Thr	Leu	Ile 115	Thr	Gln	Lys	Leu 120	Ser	Lys	Leu	Asn	Gly	Ser 125	Glu	Gly	Leu
Lys	Glu 130	Lys	Ile	Ala	Ala	Ala 135	Lys	Lys	Cys	Ser	Glu 140	Glu	Phe	Ser	Thr
Lys 145	Leu	Lys	Asp	Asn 150	His	Ala	Gln	Leu	Gly 155	Ile	Gln	Gly	Val	Thr 160	Asp
Glu	Asn	Ala	Lys 165	Lys	Ala	Ile	Leu	Lys	Ala 170	Asn	Ala	Ala	Gly	Lys 175	Asp
Lys	Gly	Val 180	Glu	Glu	Leu	Glu	Lys 185	Leu	Ser	Gly	Ser	Leu 190	Glu	Ser	Leu
Ser	Lys	Ala 195	Ala	Lys	Glu	Met 200	Leu	Ala	Asn	Ser	Val 205	Lys	Glu	Leu	Thr
Ser	Pro 210	Val	Val	His	Gly	Asn 215	Asn	Ser	Gly	Lys	Asp 220	Gly	Asn	Thr	Ser
Ala 225	Asn	Ser	Ala	Asp 230	Glu	Ser	Val	Lys	Gly	Pro 235	Asn	Leu	Thr	Glu 240	Ile
Ser	Lys	Lys	Ile 245	Thr	Glu	Ser	Asn	Ala	Val 250	Val	Leu	Ala	Val	Lys 255	Glu
Ile	Glu	Thr 260	Leu	Leu	Ala	Ser	Ile 265	Asp	Glu	Leu	Ala	Thr 270	Lys	Ala 275	Ile
Gly	Lys	Lys 275	Ile	Gln	Gln	Asn 280	Gly	Gly	Leu	Ala	Val 285	Glu	Ala	Gly 290	His
Asn	Gly 290	Thr	Leu	Leu	Ala	Gly 295	Ala	Tyr	Thr	Ile	Ser 300	Lys	Leu	Ile	Thr
Gln 305	Lys	Leu	Asp	Gly 310	Leu	Lys	Asn	Ser	Glu	Lys 315	Leu	Lys	Glu	Lys 320	Ile
Glu	Asn	Ala	Lys 325	Lys	Cys	Ser	Glu	Asp	Phe 330	Thr	Lys	Lys	Leu	Glu 335	Gly
Glu	His 340	Ala	Gln	Leu	Gly	Ile	Glu 345	Asn	Val	Thr	Asp	Glu 350	Asn	Ala 355	Lys
Lys	Ala 355	Ile	Leu	Ile	Thr	Asp 360	Ala	Ala	Lys	Asp	Lys 365	Gly	Ala	Ala 370	Glu
Leu	Glu 370	Lys	Leu	Phe	Lys	Ala 375	Val	Glu	Asn	Leu	Ala 380	Lys	Ala	Ala 385	Lys
Glu 385	Met	Leu	Ala	Asn 390	Ser	Val	Lys	Glu	Leu						

<210> 67
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<220>
 <221> CDS
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<400> 67
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 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
 50 55 60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt 240
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu
 65 70 75 80

gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat 288
 Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn
 85 90 95

gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca 336
 Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser
 100 105 110

acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta 384
 Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu
 115 120 125

aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act 432
 Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr
 130 135 140

aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat 480
 Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp
 145 150 155 160

gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat 528
 Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp
 165 170 175

aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta	576
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu	
180 185 190	
tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca	624
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr	
195 200 205	
agc cct gtt gtc cat ggt aat aat tca aga aaa gat ggg aat gca tct	672
Ser Pro Val Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser	
210 215 220	
aca aat tct gcc gat gag tct gtt aaa ggg cct aat ctt aca gaa ata	720
Thr Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile	
225 230 235 240	
agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa	768
Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu	
245 250 255	
gtt gag acc tta ctt gca tct ata gat gaa ctt gct acc aaa gct att	816
Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile	
260 265 270	
ggt aag aaa ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac	864
Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn	
275 280 285	
aca tca ttg tta tca gga gct tat gca ata tct gac cta ata gca gaa	912
Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu	
290 295 300	
aaa tta aat gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca	960
Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr	
305 310 315 320	
gct aag caa tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat	1008
Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His	
325 330 335	
gca gtg ctt ggt ctg gac aat ctt act gat gat aat gca caa aga gct	1056
Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala	
340 345 350	
att tta aaa aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa	1104
Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu	
355 360 365	
aag tta ttt aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca	1152
Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr	
370 375 380	
tta aaa aat gct gtt aaa gag ctt aca agt cc	1184
Leu Lys Asn Ala Val Lys Glu Leu Thr Ser	
385 390	

<400>	68														
Met	Arg	Leu	Leu	Ile	Gly	Phe	Ala	Leu	Ala	Leu	Ala	Leu	Ile	Gly	Cys
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			20					25					30		
Asp	Gly	Asn	Thr	Ser	Ala	Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro
		35					40					45			
Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Asp	Ser	Asn	Ala	Val	Leu
	50					55					60				
Leu	Ala	Val	Lys	Glu	Val	Glu	Ala	Leu	Leu	Ser	Ser	Ile	Asp	Glu	Leu
65				70						75				80	
Ala	Lys	Ala	Ile	Gly	Lys	Lys	Ile	Lys	Asn	Asp	Gly	Ser	Leu	Asp	Asn
				85					90					95	
Glu	Ala	Asn	Arg	Asn	Glu	Ser	Leu	Leu	Ala	Gly	Ala	Tyr	Thr	Ile	Ser
			100				105						110		
Thr	Leu	Ile	Thr	Gln	Lys	Leu	Ser	Lys	Leu	Asn	Gly	Ser	Glu	Gly	Leu
		115					120					125			
Lys	Glu	Lys	Ile	Ala	Ala	Ala	Lys	Lys	Cys	Ser	Glu	Glu	Phe	Ser	Thr
	130					135					140				
Lys	Leu	Lys	Asp	Asn	His	Ala	Gln	Leu	Gly	Ile	Gln	Gly	Val	Thr	Asp
145				150						155					160
Glu	Asn	Ala	Lys	Lys	Ala	Ile	Leu	Lys	Ala	Asn	Ala	Ala	Gly	Lys	Asp
				165					170					175	
Lys	Gly	Val	Glu	Glu	Leu	Glu	Lys	Leu	Ser	Gly	Ser	Leu	Glu	Ser	Leu
			180					185					190		
Ser	Lys	Ala	Ala	Lys	Glu	Met	Leu	Ala	Asn	Ser	Val	Lys	Glu	Leu	Thr
		195					200					205			
Ser	Pro	Val	Val	His	Gly	Asn	Asn	Ser	Arg	Lys	Asp	Gly	Asn	Ala	Ser
	210					215					220				
Thr	Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro	Asn	Leu	Thr	Glu	Ile
225				230						235				240	
Ser	Lys	Lys	Ile	Thr	Glu	Ser	Asn	Ala	Val	Val	Leu	Ala	Val	Lys	Glu
				245					250					255	
Val	Glu	Thr	Leu	Leu	Ala	Ser	Ile	Asp	Glu	Leu	Ala	Thr	Lys	Ala	Ile
			260					265					270		
Gly	Lys	Lys	Ile	Gly	Asn	Asn	Gly	Leu	Glu	Ala	Asn	Gln	Ser	Lys	Asn
		275					280					285			
Thr	Ser	Leu	Leu	Ser	Gly	Ala	Tyr	Ala	Ile	Ser	Asp	Leu	Ile	Ala	Glu
	290				295						300				
Lys	Leu	Asn	Val	Leu	Lys	Asn	Glu	Glu	Leu	Lys	Glu	Lys	Ile	Asp	Thr
305				310						315					320
Ala	Lys	Gln	Cys	Ser	Thr	Glu	Phe	Thr	Asn	Lys	Leu	Lys	Ser	Glu	His
				325					330					335	
Ala	Val	Leu	Gly	Leu	Asp	Asn	Leu	Thr	Asp	Asp	Asn	Ala	Gln	Arg	Ala

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 <211> 1209
 <212> DNA
 <213> ospC Chimera

<220>
 <221> CDS
 <222> (1)...(1209)

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 1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
 50 55 60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt 240
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu
 65 70 75 80

gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat 288
 Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn
 85 90 95

gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca 336
 Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser
 100 105 110

acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta 384
 Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu
 115 120 125

aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act 432
 Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr
 130 135 140

aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat 480
 Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp
 145 150 155 160

gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat 528
 Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp
 165 170 175

aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta	576
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu	
180 185 190	
tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca	624
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr	
195 200 205	
agc cct gtt gtc cat ggt aat aat tca ggt ggg gat tct gca tct act	672
Ser Pro Val Val His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr	
210 215 220	
aat cct gat gag tct gca aaa gga cct aat ctt acc gta ata agc aaa	720
Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys	
225 230 235 240	
aaa att aca gat tct aat gca ttt tta ctg gct gtg aaa gaa gtt gag	768
Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu	
245 250 255	
gct ttg ctt tca tct ata gat gaa ctt tct aaa gct att ggt aaa aaa	816
Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys	
260 265 270	
ata aaa aat gat ggt act tta gat aac gaa gca aat cga aac gaa tca	864
Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser	
275 280 285	
ttg ata gca gga gct tat gaa ata tca aaa cta ata aca caa aaa tta	912
Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu	
290 295 300	
agt gta ttg aat tca gaa gaa tta aag aaa aaa att aaa gag gct aag	960
Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys	
305 310 315 320	
gat tgt tcc caa aaa ttt act act aag cta aaa gat agt cat gca gag	1008
Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu	
325 330 335	
ctt ggt ata caa agc gtt cag gat gat aat gca aaa aaa gct att tta	1056
Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu	
340 345 350	
aaa aca cat gga act aaa gac aag ggt gct aaa gaa ctt gaa gag tta	1104
Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu	
355 360 365	
ttt aaa tca cta gaa agc ttg tca aaa gca gcg caa gca gca tta act	1152
Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr	
370 375 380	
aat tca gtt aaa gag ctt aca aat cct gtt gtg gca gaa agt cca aaa	1200
Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys	
385 390 395 400	
aaa cct taa	1209

Lys Pro *

<210> 70
 <211> 402
 <212> PRT
 <213> ospC Chimera

<400> 70

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Ala	Gln	Lys	Gly	Ala	Glu	Ser	Ile	Gly	Ser	Cys	Asn	Asn	Ser	Gly	Lys
		20						25					30		
Asp	Gly	Asn	Thr	Ser	Ala	Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro
	35					40						45			
Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Asp	Ser	Asn	Ala	Val	Leu
50						55				60					
Leu	Ala	Val	Lys	Glu	Val	Glu	Ala	Leu	Leu	Ser	Ser	Ile	Asp	Glu	Leu
65					70					75				80	
Ala	Lys	Ala	Ile	Gly	Lys	Lys	Ile	Lys	Asn	Asp	Gly	Ser	Leu	Asp	Asn
				85					90					95	
Glu	Ala	Asn	Arg	Asn	Glu	Ser	Leu	Leu	Ala	Gly	Ala	Tyr	Thr	Ile	Ser
		100						105					110		
Thr	Leu	Ile	Thr	Gln	Lys	Leu	Ser	Lys	Leu	Asn	Gly	Ser	Glu	Gly	Leu
	115					120						125			
Lys	Glu	Lys	Ile	Ala	Ala	Ala	Lys	Lys	Cys	Ser	Glu	Glu	Phe	Ser	Thr
	130					135					140				
Lys	Leu	Lys	Asp	Asn	His	Ala	Gln	Leu	Gly	Ile	Gln	Gly	Val	Thr	Asp
145				150						155					160
Glu	Asn	Ala	Lys	Lys	Ala	Ile	Leu	Lys	Ala	Asn	Ala	Ala	Gly	Lys	Asp
			165						170					175	
Lys	Gly	Val	Glu	Glu	Leu	Glu	Lys	Leu	Ser	Gly	Ser	Leu	Glu	Ser	Leu
		180						185					190		
Ser	Lys	Ala	Ala	Lys	Glu	Met	Leu	Ala	Asn	Ser	Val	Lys	Glu	Leu	Thr
	195					200						205			
Ser	Pro	Val	Val	His	Gly	Asn	Asn	Ser	Gly	Gly	Asp	Ser	Ala	Ser	Thr
	210				215						220				
Asn	Pro	Asp	Glu	Ser	Ala	Lys	Gly	Pro	Asn	Leu	Thr	Val	Ile	Ser	Lys
225				230						235					240
Lys	Ile	Thr	Asp	Ser	Asn	Ala	Phe	Leu	Leu	Ala	Val	Lys	Glu	Val	Glu
			245						250					255	
Ala	Leu	Leu	Ser	Ser	Ile	Asp	Glu	Leu	Ser	Lys	Ala	Ile	Gly	Lys	Lys
		260						265					270		
Ile	Lys	Asn	Asp	Gly	Thr	Leu	Asp	Asn	Glu	Ala	Asn	Arg	Asn	Glu	Ser
		275				280						285			
Leu	Ile	Ala	Gly	Ala	Tyr	Glu	Ile	Ser	Lys	Leu	Ile	Thr	Gln	Lys	Leu
290					295						300				
Ser	Val	Leu	Asn	Ser	Glu	Glu	Leu	Lys	Lys	Lys	Ile	Lys	Glu	Ala	Lys
305				310						315					320
Asp	Cys	Ser	Gln	Lys	Phe	Thr	Thr	Lys	Leu	Lys	Asp	Ser	His	Ala	Glu
			325						330					335	
Leu	Gly	Ile	Gln	Ser	Val	Gln	Asp	Asp	Asn	Ala	Lys	Lys	Ala	Ile	Leu
			340					345					350		
Lys	Thr	His	Gly	Thr	Lys	Asp	Lys	Gly	Ala	Lys	Glu	Leu	Glu	Glu	Leu
		355				360						365			
Phe	Lys	Ser	Leu	Glu	Ser	Leu	Ser	Lys	Ala	Ala	Gln	Ala	Ala	Leu	Thr
	370					375					380				

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Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys
 385 390 395 400
 Lys Pro

<210> 71
 <211> 1179
 <212> DNA
 <213> ospC Chimera

<220>
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 <222> (1)...(1179)

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 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15
 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca gga aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30
 gat ggg aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
 Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45
 aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt 192
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val
 50 55 60
 ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt 240
 Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu
 65 70 75 80
 gct acc aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc 288
 Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala
 85 90 95
 aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct 336
 Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser
 100 105 110
 gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag 384
 Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys
 115 120 125
 gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa 432
 Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys
 130 135 140
 cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat 480
 Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp
 145 150 155 160
 aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt 528
 Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly
 165 170 175

gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys 180 185 190	576
gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro 195 200 205	624
att gtc cat ggt aat aat tca ggg aaa gat ggg aat aca tct gca aat Ile Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn 210 215 220	672
tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys 225 230 235 240	720
aaa att aca gaa tct aac gca gtt gtt ctc gcc gtg aaa gaa gtt gaa Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu 245 250 255	768
act ttg ctt aca tct ata gat gag ctt gct aaa gct att ggt aaa aaa Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys 260 265 270	816
ata aaa aac gat gtt agt tta gat aat gag gca gat cac aac gga tca Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser 275 280 285	864
tta ata tca gga gca tat tta att tca aac tta ata aca aaa aaa ata Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile 290 295 300	912
agt gca ata aaa gat tca gga gaa ttg aag gca gaa att gaa aag gct Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala 305 310 315 320	960
aag aaa tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa cac aca Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr 325 330 335	1008
gat ctt ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa gcc att Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile 340 345 350	1056
tta aaa aca aat aat gat aaa act aag ggc gct gat gaa ctt gaa aag Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys 355 360 365	1104
tta ttt gaa tca gta aaa aac ttg tca aaa gca gct aaa gag atg ctt Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met Leu 370 375 380	1152
act aat tca gtt aaa gag ctt aca agc Thr Asn Ser Val Lys Glu Leu Thr Ser 385 390	1179

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Met	Arg	Leu	Leu	Ile	Gly	Phe	Ala	Leu	Ala	Leu	Ala	Leu	Ile	Gly	Cys
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			20					25					30		
Asp	Gly	Asn	Ala	Ser	Ala	Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro
		35					40					45			
Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Glu	Ser	Asn	Ala	Val	Val
	50					55					60				
Leu	Ala	Val	Lys	Glu	Val	Glu	Thr	Leu	Leu	Ala	Ser	Ile	Asp	Glu	Leu
65					70					75					80
Ala	Thr	Lys	Ala	Ile	Gly	Lys	Lys	Ile	Gly	Asn	Asn	Gly	Leu	Glu	Ala
				85					90					95	
Asn	Gln	Ser	Lys	Asn	Thr	Ser	Leu	Leu	Ser	Gly	Ala	Tyr	Ala	Ile	Ser
			100					105					110		
Asp	Leu	Ile	Ala	Glu	Lys	Leu	Asn	Val	Leu	Lys	Asn	Glu	Glu	Leu	Lys
		115					120					125			
Glu	Lys	Ile	Asp	Thr	Ala	Lys	Gln	Cys	Ser	Thr	Glu	Phe	Thr	Asn	Lys
	130					135					140				
Leu	Lys	Ser	Glu	His	Ala	Val	Leu	Gly	Leu	Asp	Asn	Leu	Thr	Asp	Asp
145					150					155					160
Asn	Ala	Gln	Arg	Ala	Ile	Leu	Lys	Lys	His	Ala	Asn	Lys	Asp	Lys	Gly
				165					170					175	
Ala	Ala	Glu	Leu	Glu	Lys	Leu	Phe	Lys	Ala	Val	Glu	Asn	Leu	Ser	Lys
			180					185					190		
Ala	Ala	Gln	Asp	Thr	Leu	Lys	Asn	Ala	Val	Lys	Glu	Leu	Thr	Ser	Pro
		195					200					205			
Ile	Val	His	Gly	Asn	Asn	Ser	Gly	Lys	Asp	Gly	Asn	Thr	Ser	Ala	Asn
	210					215					220				
Ser	Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro	Asn	Leu	Thr	Glu	Ile	Ser	Lys
225					230					235					240
Lys	Ile	Thr	Glu	Ser	Asn	Ala	Val	Val	Leu	Ala	Val	Lys	Glu	Val	Glu
				245					250					255	
Thr	Leu	Leu	Thr	Ser	Ile	Asp	Glu	Leu	Ala	Lys	Ala	Ile	Gly	Lys	Lys
			260					265					270		
Ile	Lys	Asn	Asp	Val	Ser	Leu	Asp	Asn	Glu	Ala	Asp	His	Asn	Gly	Ser
		275					280					285			
Leu	Ile	Ser	Gly	Ala	Tyr	Leu	Ile	Ser	Asn	Leu	Ile	Thr	Lys	Lys	Ile
	290					295					300				
Ser	Ala	Ile	Lys	Asp	Ser	Gly	Glu	Leu	Lys	Ala	Glu	Ile	Glu	Lys	Ala
305				310						315					320
Lys	Lys	Cys	Ser	Glu	Glu	Phe	Thr	Ala	Lys	Leu	Lys	Gly	Glu	His	Thr
				325					330					335	
Asp	Leu	Gly	Lys	Glu	Gly	Val	Thr	Asp	Asp	Asn</					

<210> 73
 <211> 1178
 <212> DNA
 <213> ospC Chimera

<220>
 <221> CDS
 <222> (1)...(1178)

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 atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15
 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca gga aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30
 gat ggg aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
 Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45
 aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt 192
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val
 50 55 60
 ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt 240
 Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu
 65 70 75 80
 gct acc aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc 288
 Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala
 85 90 95
 aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct 336
 Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser
 100 105 110
 gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag 384
 Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys
 115 120 125
 gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa 432
 Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys
 130 135 140
 cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat 480
 Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp
 145 150 155 160
 aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt 528
 Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly
 165 170 175

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gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys 180 185 190	576
gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro 195 200 205	624
att gtc cat ggt aat aat tca gga aaa gat ggg aat aca tct gca aat Ile Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn 210 215 220	672
tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys 225 230 235 240	720
aaa att aca gaa tct aac gca gtt gtt ctg gct gtg aaa gaa att gaa Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu 245 250 255	768
act ttg ctt gca tct ata gat gaa ctt gct act aaa gct att ggt aaa Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys 260 265 270	816
aaa ata caa caa aat ggt ggt tta gct gtc gaa gcg ggg cat aat gga Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly 275 280 285	864
aca ttg tta gca ggt gct tat aca ata tca aaa cta ata aca caa aaa Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys 290 295 300	912
tta gat gga ttg aaa aat tca gaa aaa tta aag gaa aaa att gaa aat Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn 305 310 315 320	960
gct aag aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga gaa cat Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His 325 330 335	1008
gcg caa ctt gga att gaa aat gtt act gat gag aat gca aaa aaa gct Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala 340 345 350	1056
att tta ata aca gat gca gct aaa gat aag ggc gct gca gag ctt gaa Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu 355 360 365	1104
aag cta ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa gag atg Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met 370 375 380	1152
ctt gct aat tca gtt aaa gag ctt ac Leu Ala Asn Ser Val Lys Glu Leu 385 390	1178

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Ala	Gln	Lys	Gly 20	Ala	Glu	Ser	Ile	Gly 25	Ser	Cys	Asn	Asn	Ser 30	Gly	Lys
Asp	Gly	Asn 35	Ala	Ser	Ala	Asn	Ser 40	Ala	Asp	Glu	Ser	Val 45	Lys	Gly	Pro
Asn	Leu 50	Thr	Glu	Ile	Ser	Lys 55	Lys	Ile	Thr	Glu	Ser 60	Asn	Ala	Val	Val
Leu 65	Ala	Val	Lys	Glu	Val 70	Glu	Thr	Leu	Leu	Ala 75	Ser	Ile	Asp	Glu	Leu 80
Ala	Thr	Lys	Ala	Ile 85	Gly	Lys	Lys	Ile	Gly 90	Asn	Asn	Gly	Leu 95	Glu	Ala
Asn	Gln	Ser	Lys 100	Asn	Thr	Ser	Leu	Leu 105	Ser	Gly	Ala	Tyr	Ala 110	Ile	Ser
Asp	Leu	Ile 115	Ala	Glu	Lys	Leu	Asn 120	Val	Leu	Lys	Asn	Glu 125	Glu	Leu	Lys
Glu	Lys 130	Ile	Asp	Thr	Ala	Lys 135	Gln	Cys	Ser	Thr	Glu 140	Phe	Thr	Asn	Lys
Leu 145	Lys	Ser	Glu	His 150	Ala	Val	Leu	Gly	Leu	Asp 155	Asn	Leu	Thr	Asp	Asp 160
Asn	Ala	Gln	Arg	Ala 165	Ile	Leu	Lys	Lys	His 170	Ala	Asn	Lys	Asp	Lys	Gly
Ala	Ala	Glu	Leu 180	Glu	Lys	Leu	Phe	Lys 185	Ala	Val	Glu	Asn	Leu 190	Ser	Lys
Ala	Ala	Gln 195	Asp	Thr	Leu	Lys	Asn 200	Ala	Val	Lys	Glu	Leu 205	Thr	Ser	Pro
Ile	Val 210	His	Gly	Asn	Asn	Ser 215	Gly	Lys	Asp	Gly	Asn 220	Thr	Ser	Ala	Asn
Ser 225	Ala	Asp	Glu	Ser	Val 230	Lys	Gly	Pro	Asn	Leu 235	Thr	Glu	Ile	Ser	Lys 240
Lys	Ile	Thr	Glu	Ser 245	Asn	Ala	Val	Val	Leu 250	Ala	Val	Lys	Glu	Ile	Glu 255
Thr	Leu	Leu	Ala 260	Ser	Ile	Asp	Glu	Leu 265	Ala	Thr	Lys	Ala	Ile 270	Gly	Lys
Lys	Ile	Gln 275	Gln	Asn	Gly	Gly	Leu 280	Ala	Val	Glu	Ala	Gly 285	His	Asn	Gly
Thr	Leu 290	Leu	Ala	Gly	Ala	Tyr 295	Thr	Ile	Ser	Lys	Leu 300	Ile	Thr	Gln	Lys
Leu 305	Asp	Gly	Leu	Lys	Asn 310	Ser	Glu	Lys	Leu	Lys 315	Glu	Lys	Ile	Glu	Asn 320
Ala	Lys	Lys	Cys	Ser 325	Glu	Asp	Phe	Thr	Lys 330	Lys	Leu	Glu	Gly	Glu	His 335
Ala	Gln	Leu	Gly 340	Ile	Glu	Asn	Val	Thr 345	Asp	Glu	Asn	Ala	Lys 350	Lys	Ala
Ile	Leu 355	Ile	Thr	Asp	Ala	Ala	Lys 360	Asp	Lys	Gly	Ala	Ala 365	Glu	Leu	Glu
Lys	Leu 370	Phe	Lys	Ala	Val	Glu 375	Asn	Leu	Ala	Lys	Ala 380	Ala	Lys	Glu	Met
Leu 385	Ala	Asn	Ser	Val	Lys 390	Glu	Leu								

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 1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca gga aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30

gat ggg aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
 Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45

aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt 192
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val
 50 55 60

ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt 240
 Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu
 65 70 75 80

gct acc aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc 288
 Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala
 85 90 95

aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct 336
 Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser
 100 105 110

gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag 384
 Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys
 115 120 125

gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa 432
 Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys
 130 135 140

cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat 480
 Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp
 145 150 155 160

aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt 528
 Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly
 165 170 175

gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa 576
 Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys
 180 185 190

gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct	624
Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro	
195 200 205	
att gtc cat ggt aat aat tca aga aaa gat ggg aat gca tct aca aat	672
Ile Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser Thr Asn	
210 215 220	
tct gcc gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa	720
Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys	
225 230 235 240	
aaa att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa gtt gag	768
Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu	
245 250 255	
acc tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aag	816
Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys	
260 265 270	
aaa ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca	864
Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser	
275 280 285	
ttg tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta	912
Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu	
290 295 300	
aat gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag	960
Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys	
305 310 315 320	
caa tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat gca gtg	1008
Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val	
325 330 335	
ctt ggt ctg gac aat ctt act gat gat aat gca caa aga gct att tta	1056
Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu	
340 345 350	
aaa aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa aag tta	1104
Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu	
355 360 365	
ttt aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa	1152
Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys	
370 375 380	
aat gct gtt aaa gag ctt aca agt cc	1178
Asn Ala Val Lys Glu Leu Thr Ser	
385 390	

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Ala	Gln	Lys	Gly 20	Ala	Glu	Ser	Ile	Gly 25	Ser	Cys	Asn	Asn	Ser 30	Gly	Lys
Asp	Gly	Asn 35	Ala	Ser	Ala	Asn 40	Ser	Ala	Asp	Glu	Ser 45	Val	Lys	Gly	Pro
Asn 50	Leu	Thr	Glu	Ile	Ser	Lys 55	Lys	Ile	Thr	Glu	Ser 60	Asn	Ala	Val	Val
Leu 65	Ala	Val	Lys	Glu	Val 70	Glu	Thr	Leu	Leu	Ala 75	Ser	Ile	Asp	Glu	Leu 80
Ala	Thr	Lys	Ala	Ile 85	Gly	Lys	Lys	Ile	Gly 90	Asn	Asn	Gly	Leu 95	Glu	Ala
Asn	Gln	Ser	Lys 100	Asn	Thr	Ser	Leu	Leu 105	Ser	Gly	Ala	Tyr	Ala 110	Ile	Ser
Asp	Leu	Ile 115	Ala	Glu	Lys	Leu	Asn 120	Val	Leu	Lys	Asn	Glu 125	Glu	Leu	Lys
Glu	Lys 130	Ile	Asp	Thr	Ala	Lys 135	Gln	Cys	Ser	Thr	Glu 140	Phe	Thr	Asn	Lys
Leu 145	Lys	Ser	Glu	His 150	Ala	Val	Leu	Gly	Leu	Asp 155	Asn	Leu	Thr	Asp	Asp 160
Asn	Ala	Gln	Arg	Ala 165	Ile	Leu	Lys	Lys	His 170	Ala	Asn	Lys	Asp	Lys 175	Gly
Ala	Ala	Glu	Leu 180	Glu	Lys	Leu	Phe	Lys 185	Ala	Val	Glu	Asn	Leu 190	Ser	Lys
Ala	Ala	Gln 195	Asp	Thr	Leu	Lys	Asn 200	Ala	Val	Lys	Glu	Leu 205	Thr	Ser	Pro
Ile	Val 210	His	Gly	Asn	Asn	Ser 215	Arg	Lys	Asp	Gly	Asn	Ala	Ser	Thr	Asn
Ser 225	Ala	Asp	Glu	Ser	Val	Lys 230	Gly	Pro	Asn	Leu	Thr	Glu	Ile	Ser	Lys
Lys	Ile	Thr	Glu	Ser 245	Asn	Ala	Val	Val	Leu	Ala	Val	Lys	Glu	Val	Glu
Thr	Leu	Leu	Ala 260	Ser	Ile	Asp	Glu	Leu 265	Ala	Thr	Lys	Ala	Ile	Gly	Lys
Lys	Ile	Gly 275	Asn	Asn	Gly	Leu	Glu	Ala 280	Asn	Gln	Ser	Lys	Asn	Thr	Ser
Leu	Leu	Ser	Gly	Ala	Tyr	Ala 295	Ile	Ser	Asp	Leu	Ile	Ala	Glu	Lys	Leu
Asn 305	Val	Leu	Lys	Asn	Glu	Leu	Lys	Glu	Lys	Leu	Ile	Asp	Thr	Ala	Lys
Gln	Cys	Ser	Thr	Glu 325	Phe	Thr	Asn	Lys	Leu	Lys	Ser	Glu	His	Ala	Val
Leu	Gly	Leu	Asp 340	Asn	Leu	Thr	Asp	Asp	Asn	Ala	Gln	Arg	Ala	Ile	Leu
Lys	Lys	His 355	Ala	Asn	Lys	Asp	Lys	Gly	Ala	Ala	Glu	Leu	Glu	Lys	Leu
Phe	Lys 370	Ala	Val	Glu	Asn	Leu	Ser	Lys	Ala	Ala	Gln	Asp	Thr	Leu	Lys
Asn 385	Ala	Val	Lys	Glu	Leu	Thr	Ser								

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 1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
 50 55 60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile
 65 70 75 80

gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288
 Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp
 85 90 95

acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata 336
 Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile
 100 105 110

tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta 384
 Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu
 115 120 125

aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat 432
 Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn
 130 135 140

aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat 480
 Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp
 145 150 155 160

gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa 528
 Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys
 165 170 175

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ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca	576
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser	
180 185 190	
aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc	624
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser	
195 200 205	
cct gtt gtg gca gaa agt cca aaa aaa cct ttc cat ggt aat aat tca	672
Pro Val Val Ala Glu Ser Pro Lys Lys Pro Phe His Gly Asn Asn Ser	
210 215 220	
ggt ggg gat tct gca tct act aat cct gat gag tct gca aaa gga cct	720
Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly Pro	
225 230 235 240	
aat ctt acc gta ata agc aaa aaa att aca gat tct aat gca ttt tta	768
Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe Leu	
245 250 255	
ctg gct gtg aaa gaa gtt gag gct ttg ctt tca tct ata gat gaa ctt	816
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu	
260 265 270	
tct aaa gct att ggt aaa aaa ata aaa aat gat ggt act tta gat aac	864
Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp Asn	
275 280 285	
gaa gca aat cga aac gaa tca ttg ata gca gga gct tat gaa ata tca	912
Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile Ser	
290 295 300	
aaa cta ata aca caa aaa tta agt gta ttg aat tca gaa gaa tta aag	960
Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu Lys	
305 310 315 320	
aaa aaa att aaa gag gct aag gat tgt tcc caa aaa ttt act act aag	1008
Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr Lys	
325 330 335	
cta aaa gat agt cat gca gag ctt ggt ata caa agc gtt cag gat gat	1056
Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp Asp	
340 345 350	
aat gca aaa aaa gct att tta aaa aca cat gga act aaa gac aag ggt	1104
Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys Gly	
355 360 365	
gct aaa gaa ctt gaa gag tta ttt aaa tca cta gaa agc ttg tca aaa	1152
Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser Lys	
370 375 380	
gca gcg caa gca gca tta act aat tca gtt aaa gag ctt aca aat cct	1200
Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn Pro	
385 390 395 400	

gtt gtg gca gaa agt cca aaa aaa cct taa
 Val Val Ala Glu Ser Pro Lys Lys Pro *
 405

1230

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 35 40 45
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
 50 55 60
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile
 65 70 75 80
 Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp
 85 90 95
 Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile
 100 105 110
 Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu
 115 120 125
 Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn
 130 135 140

 Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp
 145 150 155 160
 Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys
 165 170 175
 Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser
 180 185 190
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
 195 200 205
 Pro Val Val Ala Glu Ser Pro Lys Lys Pro Phe His Gly Asn Asn Ser
 210 215 220
 Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly Pro
 225 230 235 240
 Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe Leu
 245 250 255
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu
 260 265 270
 Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp Asn
 275 280 285
 Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile Ser
 290 295 300
 Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu Lys
 305 310 315 320
 Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr Lys
 325 330 335
 Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp Asp
 340 345 350

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Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys Gly
 355 360 365
 Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser Lys
 370 375 380
 Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn Pro
 385 390 395 400
 Val Val Ala Glu Ser Pro Lys Lys Pro
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gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
 50 55 60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile
 65 70 75 80

gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288
 Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp
 85 90 95

acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata 336
 Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile
 100 105 110

tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta 384
 Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu
 115 120 125

aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat 432
 Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn
 130 135 140

aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat 480

99/108

Lys 145	Leu	Lys	Glu	Lys	His 150	Thr	Asp	Leu	Gly	Lys 155	Glu	Gly	Val	Thr	Asp 160	
gct Ala	gat Asp	gca Ala	aaa Lys	gaa Glu	gcc Ala	att Ile	tta Leu	aaa Lys	aca Thr	aat Asn	ggg Gly	act Thr	aaa Lys	act Thr	aaa Lys	528
				165					170							
ggg Gly	gct Ala	gaa Glu	gaa Glu	ctt Leu	gga Gly	aaa Lys	tta Leu	ttt Phe	gaa Glu	tca Ser	gta Val	gag Glu	gtc Val	ttg Leu	tca Ser	576
			180					185					190			
aaa Lys	gca Ala	gct Ala	aaa Lys	gag Glu	atg Met	ctt Leu	gct Ala	aat Asn	tca Ser	gtt Val	aaa Lys	gag Glu	ctt Leu	aca Thr	agc Ser	624
			195				200					205				
cct Pro	gtt Val	gtg Val	gca Ala	gaa Glu	agt Ser	cca Pro	aaa Lys	aaa Lys	cct Pro	tcc Ser	atg Met	gta Val	aat Asn	aat Asn	tca Ser	672
	210					215					220					
ggg Gly	aaa Lys	gat Asp	ggg Gly	aat Asn	aca Thr	tct Ser	gca Ala	aat Asn	tct Ser	gct Ala	gat Asp	gag Glu	tct Ser	gtt Val	aaa Lys	720
225					230				235						240	
ggg Gly	cct Pro	aat Asn	ctt Leu	aca Thr	gaa Glu	ata Ile	agt Ser	aaa Lys	aaa Lys	att Ile	aca Thr	gaa Glu	tct Ser	aac Asn	gca Ala	768
				245					250					255		
gtt Val	gtt Val	ctc Leu	gcc Ala	gtg Val	aaa Lys	gaa Glu	gtt Val	gaa Glu	act Thr	ttg Leu	ctt Leu	aca Thr	tct Ser	ata Ile	gat Asp	816
			260					265					270			
gag Glu	ctt Leu	gct Ala	aaa Lys	gct Ala	att Ile	ggg Gly	aaa Lys	aaa Lys	ata Ile	aaa Lys	aac Asn	gat Asp	gtt Val	agt Ser	tta Leu	864
			275				280					285				
gat Asp	aat Asn	gag Glu	gca Ala	gat Asp	cac His	aac Asn	gga Gly	tca Ser	tta Leu	ata Ile	tca Ser	gga Gly	gca Ala	tat Tyr	tta Leu	912
	290					295					300					
att Ile	tca Ser	aac Asn	tta Leu	ata Ile	aca Thr	aaa Lys	aaa Lys	ata Ile	agt Ser	gca Ala	ata Ile	aaa Lys	gat Asp	tca Ser	gga Gly	960
305					310					315					320	
gaa Glu	ttg Leu	aag Lys	gca Ala	gaa Glu	att Ile	gaa Glu	aag Lys	gct Ala	aag Lys	aaa Lys	tgt Cys	tct Ser	gaa Glu	gaa Glu	ttt Phe	1008
				325				330						335		
act Thr	gct Ala	aaa Lys	tta Leu	aaa Lys	ggg Gly	gaa Glu	cac His	aca Thr	gat Asp	ctt Leu	ggg Gly	aaa Lys	gaa Glu	ggc Gly	gtt Val	1056
			340					345					350			
act Thr	gat Asp	gat Asp	aat Asn	gca Ala	aaa Lys	aaa Lys	gcc Ala	att Ile	tta Leu	aaa Lys	aca Thr	aat Asn	aat Asn	gat Asp	aaa Lys	1104
			355				360					365				

100/108

act aag ggc gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac 1152
 Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn
 370 375 380

ttg tca aaa gca gct aaa gag atg ctt act aat tca gtt aaa gag ctt 1200
 Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu
 385 390 395 400

aca agc taa 1209
 Thr Ser *

<210> 80
 <211> 402
 <212> PRT
 <213> ospC Chimera

<400> 80
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
 50 55 60
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile
 65 70 75 80
 Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp
 85 90 95
 Thr Glu Tyr Asn His Asn Gly Ser Leu Ala Gly Ala Tyr Ala Ile
 100 105 110
 Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu
 115 120 125
 Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn
 130 135 140
 Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp
 145 150 155 160
 Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys
 165 170 175
 Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser
 180 185 190
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
 195 200 205
 Pro Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser
 210 215 220
 Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys
 225 230 235 240
 Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala
 245 250 255
 Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp
 260 265 270
 Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu
 275 280 285
 Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu
 290 295 300

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Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly
 305 310 315 320
 Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe
 325 330 335
 Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val
 340 345 350
 Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys
 355 360 365
 Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn
 370 375 380
 Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu
 385 390 395 400
 Thr Ser

<210> 81
 <211> 1205
 <212> DNA
 <213> ospC Chimera

<220>
 <221> CDS
 <222> (1)...(1205)

<400> 81
 atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15

 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30

 gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45

 aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
 50 55 60

 ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile
 65 70 75 80

 gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288
 Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp
 85 90 95

 acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata 336
 Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile
 100 105 110
 tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta 384
 Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu
 115 120 125

102/108

aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat	432
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn	
130 135 140	
aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat	480
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp	
145 150 155 160	
gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa	528
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys	
165 170 175	
ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca	576
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser	
180 185 190	
aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc	624
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser	
195 200 205	
cct gtt gtg gca gaa agt cca aaa aaa cct tcc atg gta aat aat tca	672
Pro Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser	
210 215 220	
gga aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa	720
Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys	
225 230 235 240	
ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca	768
Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala	
245 250 255	
gtt gtt ctg gct gtg aaa gaa att gaa act ttg ctt gca tct ata gat	816
Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp	
260 265 270	
gaa ctt gct act aaa gct att ggt aaa aaa ata caa caa aat ggt ggt	864
Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly	
275 280 285	
tta gct gtc gaa gcg ggg cat aat gga aca ttg tta gca ggt gct tat	912
Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr	
290 295 300	
aca ata tca aaa cta ata aca caa aaa tta gat gga ttg aaa aat tca	960
Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser	
305 310 315 320	
gaa aaa tta aag gaa aaa att gaa aat gct aag aaa tgt tct gaa gat	1008
Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp	
325 330 335	
ttt act aaa aaa cta gaa gga gaa cat gcg caa ctt gga att gaa aat	1056
Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn	
340 345 350	

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gtt act gat gag aat gca aaa aaa gct att tta ata aca gat gca gct 1104
Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala
      355                      360                      365

aaa gat aag ggc gct gca gag ctt gaa aag cta ttt aaa gca gta gaa 1152
Lys Asp Lys Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu
      370                      375                      380

aac ttg gca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag 1200
Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu
      385                      390                      395                      400

ctt ac
Leu
1205

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<210> 82
<211> 401
<212> PRT
<213> ospC Chimera

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<400> 82
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1      5      10      15
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20      25      30
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35      40      45
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
 50      55      60
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile
 65      70      75      80
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp
 85      90      95
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile
100      105      110
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu
115      120      125
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn
130      135      140
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp
145      150      155      160
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys
165      170      175
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser
180      185      190
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
195      200      205
Pro Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser
210      215      220
Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys
225      230      235      240
Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala
245      250      255
Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp
260      265      270

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Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly
 275 280 285
 Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr
 290 295 300
 Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser
 305 310 315
 Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp
 325 330 335
 Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn
 340 345 350
 Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala
 355 360 365
 Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu
 370 375 380
 Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu
 385 390 395 400
 Leu

<210> 83
 <211> 1236
 <212> DNA
 <213> ospC Chimera

<220>
 <221> CDS
 <222> (1)...(1236)

<400> 83
 atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15

 gca caa aaa ggt gct gag tca att gga tcc tgt agt aat tca ggg aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Ser Asn Ser Gly Lys
 20 25 30

 ggt ggg gat tct gca tct act aat cct gct gac gag tct gcg aaa ggg 144
 Gly Gly Asp Ser Ala Ser Thr Asn Pro Ala Asp Glu Ser Ala Lys Gly
 35 40 45

 cct aat ctt aca gaa ata agc aaa aaa att aca gat tct aat gca ttt 192
 Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe
 50 55 60

 gta ctt gct gtt aaa gaa gtt gag act ttg gtt tta tct ata gat gaa 240
 Val Leu Ala Val Lys Glu Val Glu Thr Leu Val Leu Ser Ile Asp Glu
 65 70 75 80

 ctt gct aag aaa gct att ggt caa aaa ata gac aat aat aat ggt tta 288
 Leu Ala Lys Lys Ala Ile Gly Gln Lys Ile Asp Asn Asn Asn Gly Leu
 85 90 95

 gct gct tta aat aat cag aat gga tcg ttg tta gca gga gcc tat gca 336
 Ala Ala Leu Asn Asn Gln Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala
 100 105 110

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ata tca acc cta ata aca gaa aaa ttg agt aaa ttg aaa aat tta gaa Ile Ser Thr Leu Ile Thr Glu Lys Leu Ser Lys Leu Lys Asn Leu Glu 115 120 125	384
gaa tta aag aca gaa att gca aag gct aag aaa tgt tcc gaa gaa ttt Glu Leu Lys Thr Glu Ile Ala Lys Ala Lys Lys Cys Ser Glu Glu Phe 130 135 140	432
act aat aaa cta aaa agt ggt cat gca gat ctt ggc aaa cag gat gct Thr Asn Lys Leu Lys Ser Gly His Ala Asp Leu Gly Lys Gln Asp Ala 145 150 155 160	480
acc gat gat cat gca aaa gca gct att tta aaa aca cat gca act acc Thr Asp Asp His Ala Lys Ala Ala Ile Leu Lys Thr His Ala Thr Thr 165 170 175	528
gat aaa ggt gct aaa gaa ttt aaa gat tta ttt gaa tca gta gaa ggt Asp Lys Gly Ala Lys Glu Phe Lys Asp Leu Phe Glu Ser Val Glu Gly 180 185 190	576
ttg tta aaa gca gct caa gta gca cta act aat tca gtt aaa gaa ctt Leu Leu Lys Ala Ala Gln Val Ala Leu Thr Asn Ser Val Lys Glu Leu 195 200 205	624
aca agt cct gtt gta gca gaa agt cca aaa aaa cct cat atg gct aat Thr Ser Pro Val Val Ala Glu Ser Pro Lys Lys Pro His Met Ala Asn 210 215 220	672
aat tca ggt ggg gat tct gca tct act aat cct gat gag tct gca aaa Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys 225 230 235 240	720
gga cct aat ctt acc gta ata agc aaa aaa att aca gat tct aat gca Gly Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala 245 250 255	768
ttt tta ctg gct gtg aaa gaa gtt gag gct ttg ctt tca tct ata gat Phe Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp 260 265 270	816
gaa ctt tct aaa gct att ggt aaa aaa ata aaa aat gat ggt act tta Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu 275 280 285	864
gat aac gaa gca aat cga aac gaa tca ttg ata gca gga gct tat gaa Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu 290 295 300	912
ata tca aaa cta ata aca caa aaa tta agt gta ttg aat tca gaa gaa Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu 305 310 315 320	960
tta aag aaa aaa att aaa gag gct aag gat tgt tcc caa aaa ttt act Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr 325 330 335	1008
act aag cta aaa gat agt cat gca gag ctt ggt ata caa agc gtt cag	1056

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Thr	Lys	Leu	Lys	Asp	Ser	His	Ala	Glu	Leu	Gly	Ile	Gln	Ser	Val	Gln		
			340					345					350				
gat	gat	aat	gca	aaa	aaa	gct	att	tta	aaa	aca	cat	gga	act	aaa	gac	1104	
Asp	Asp	Asn	Ala	Lys	Lys	Ala	Ile	Leu	Lys	Thr	His	Gly	Thr	Lys	Asp		
		355				360						365					
aag	ggt	gct	aaa	gaa	ctt	gaa	gag	tta	ttt	aaa	tca	cta	gaa	agc	ttg	1152	
Lys	Gly	Ala	Lys	Glu	Leu	Glu	Glu	Leu	Phe	Lys	Ser	Leu	Glu	Ser	Leu		
	370					375					380						
tca	aaa	gca	gca	caa	gca	gca	tta	act	aat	tca	gtt	aaa	gag	ctt	aca	1200	
Ser	Lys	Ala	Ala	Gln	Ala	Ala	Leu	Thr	Asn	Ser	Val	Lys	Glu	Leu	Thr		
	385				390					395					400		
aat	cct	gtt	gtg	gca	gaa	agt	cca	aaa	aaa	cct	tta					1236	
Asn	Pro	Val	Val	Ala	Glu	Ser	Pro	Lys	Lys	Pro	*						
				405					410								

<210> 84

<211> 411

<212> PRT

<213> ospC Chimera

<400> 84

Met	Arg	Leu	Leu	Ile	Gly	Phe	Ala	Leu	Ala	Leu	Ala	Leu	Ile	Gly	Cys		
1				5					10					15			
Ala	Gln	Lys	Gly	Ala	Glu	Ser	Ile	Gly	Ser	Cys	Ser	Asn	Ser	Gly	Lys		
		20						25				30					
Gly	Gly	Asp	Ser	Ala	Ser	Thr	Asn	Pro	Ala	Asp	Glu	Ser	Ala	Lys	Gly		
		35					40					45					
Pro	Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Asp	Ser	Asn	Ala	Phe		
	50					55					60						
Val	Leu	Ala	Val	Lys	Glu	Val	Glu	Thr	Leu	Val	Leu	Ser	Ile	Asp	Glu		
	65				70					75					80		
Leu	Ala	Lys	Lys	Ala	Ile	Gly	Gln	Lys	Ile	Asp	Asn	Asn	Asn	Gly	Leu		
				85					90					95			
Ala	Ala	Leu	Asn	Asn	Gln	Asn	Gly	Ser	Leu	Leu	Ala	Gly	Ala	Tyr	Ala		
		100						105					110				
Ile	Ser	Thr	Leu	Ile	Thr	Glu	Lys	Leu	Ser	Lys	Leu	Lys	Asn	Leu	Glu		
		115				120						125					
Glu	Leu	Lys	Thr	Glu	Ile	Ala	Lys	Ala	Lys	Lys	Cys	Ser	Glu	Glu	Phe		
	130					135					140						
Thr	Asn	Lys	Leu	Lys	Ser	Gly	His	Ala	Asp	Leu	Gly	Lys	Gln	Asp	Ala		
	145				150					155					160		
Thr	Asp	Asp	His	Lys	Ala	Ala	Ile	Leu	Lys	Thr	His	Ala	Thr	Thr			
			165					170						175			
Asp	Lys	Gly	Ala	Lys	Glu	Phe	Lys	Asp	Leu	Phe	Glu	Ser	Val	Glu	Gly		
		180						185					190				
Leu	Leu	Lys	Ala	Ala	Gln	Val	Ala	Leu	Thr	Asn	Ser	Val	Lys	Glu	Leu		
		195					200					205					
Thr	Ser	Pro	Val	Val	Ala	Glu	Ser	Pro	Lys	Lys	Pro	His	Met	Ala	Asn		
	210					215					220						
Asn	Ser	Gly	Gly	Asp	Ser	Ala	Ser	Thr	Asn	Pro	Asp	Glu	Ser	Ala	Lys		
	225				230					235					240		

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<210> 85
<211> 192
<212> PRT
<213> borrelia burgdorferi
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<400>	85														
Cys 1	Asn	Asn	Ser	Gly 5	Lys	Asp	Gly	Asn	Thr 10	Ser	Ala	Asn	Ser	Ala	Asp
Glu	Ser	Val	Lys 20	Gly	Pro	Asn	Leu	Thr 25	Glu	Ile	Ser	Lys	Lys 30	Ile	Thr
Glu	Ser	Asn 35	Ala	Val	Val	Leu	Ala 40	Val	Lys	Glu	Val	Glu 45	Thr	Leu	Leu
Thr	Ser 50	Ile	Asp	Glu	Leu	Ala 55	Lys	Ala	Ile	Gly	Lys 60	Lys	Ile	Lys	Asn
Asp 65	Val	Ser	Leu	Asp	Asn 70	Glu	Ala	Asp	His	Asn 75	Gly	Ser	Leu	Ile	Ser 80
Gly	Ala	Tyr	Leu 85	Ile	Ser	Thr	Leu	Ile 90	Thr	Lys	Lys	Ile	Ser 95	Ala	Ile
Lys	Asp	Ser	Gly 100	Glu	Leu	Lys	Ala	Glu 105	Ile	Glu	Lys	Ala	Lys 110	Lys	Cys
Ser	Glu	Glu 115	Phe	Thr	Ala	Lys	Leu 120	Lys	Gly	Glu	His	Thr 125	Asp	Leu	Gly
Lys	Glu 130	Gly	Val	Thr	Asp	Asp 135	Asn	Ala	Lys	Lys	Ala 140	Ile	Leu	Lys	Thr
Asn 145	Asn	Asp	Lys	Thr	Lys 150	Gly	Ala	Asp	Glu	Leu 155	Glu	Lys	Leu	Phe	Glu 160
Ser	Val	Lys	Asn 165	Leu	Ser	Lys	Ala	Ala 170	Lys	Glu	Met	Leu	Thr 175	Asn	Ser
Val	Lys	Glu	Leu 180	Thr	Ser	Pro	Val	Val 185	Ala	Glu	Ser	Pro	Lys 190	Lys	Pro

<210> 86
 <211> 191
 <212> PRT
 <213> borrelia burgdorferi

<400> 86

Asn	Ser	Gly	Lys	Gly	Gly	Asn	Thr	Ser	Ala	Asn	Ser	Ala	Asp	Glu	Ser
1				5					10					15	
Val	Lys	Gly	Pro	Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Glu	Ser
			20					25					30		
Asn	Ala	Val	Val	Leu	Ala	Val	Lys	Glu	Ile	Glu	Thr	Leu	Leu	Ala	Ser
			35					40					45		
Ile	Asp	Glu	Leu	Ala	Thr	Lys	Ala	Ile	Gly	Lys	Lys	Ile	Gln	Gln	Asn
	50					55					60				
Gly	Gly	Leu	Ala	Val	Glu	Ala	Gly	His	Asn	Gly	Thr	Leu	Leu	Ala	Gly
65					70					75					80
Ala	Tyr	Thr	Ile	Ser	Lys	Leu	Ile	Thr	Gln	Lys	Leu	Asp	Gly	Leu	Lys
				85					90					95	
Asn	Ser	Glu	Lys	Leu	Lys	Glu	Lys	Ile	Glu	Asn	Ala	Lys	Lys	Cys	Ser
			100					105					110		
Glu	Asp	Phe	Thr	Lys	Lys	Leu	Glu	Gly	Glu	His	Ala	Gln	Leu	Gly	Ile
	115					120						125			
Glu	Asn	Val	Thr	Asp	Glu	Asn	Ala	Lys	Lys	Ala	Ile	Leu	Ile	Thr	Asp
	130					135					140				
Ala	Ala	Lys	Asp	Lys	Gly	Ala	Ala	Glu	Leu	Glu	Lys	Leu	Phe	Lys	Ala
145					150					155					160
Val	Glu	Asn	Leu	Ala	Lys	Ala	Ala	Lys	Glu	Met	Leu	Ala	Asn	Ser	Val
				165					170					175	
Lys	Glu	Leu	Thr	Ser	Pro	Ile	Val	Ala	Glu	Ser	Pro	Lys	Lys	Pro	
			180					185					190		